

1/50

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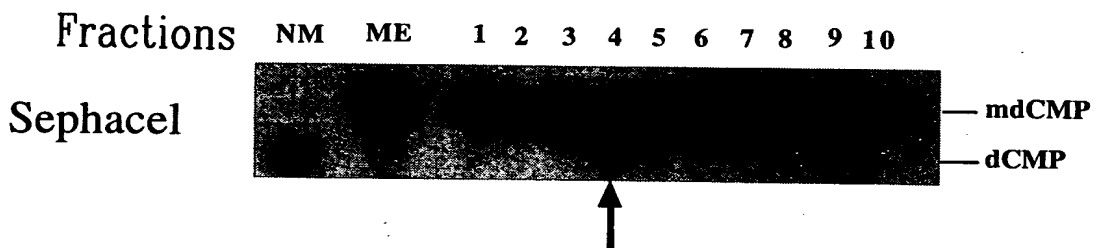
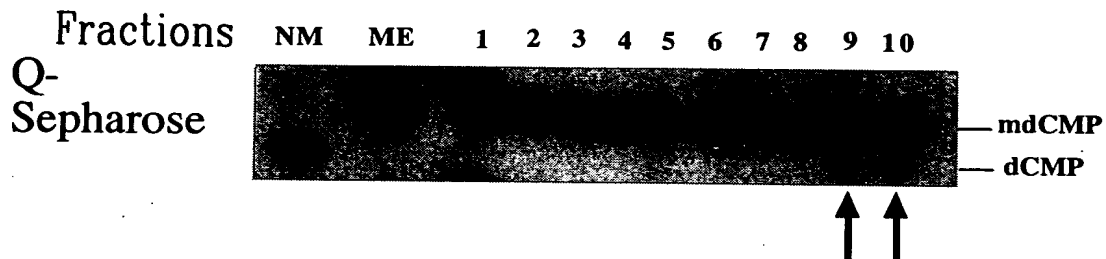
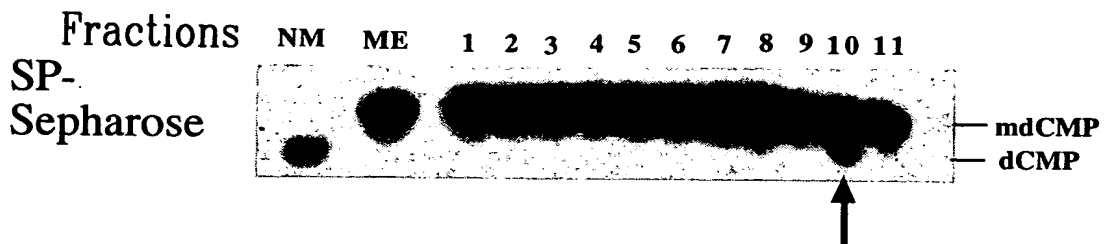
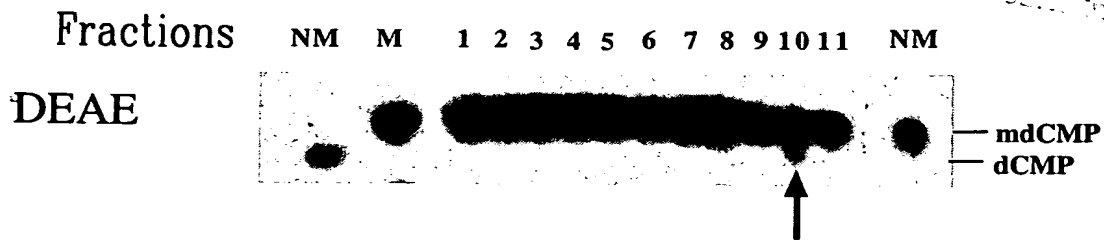
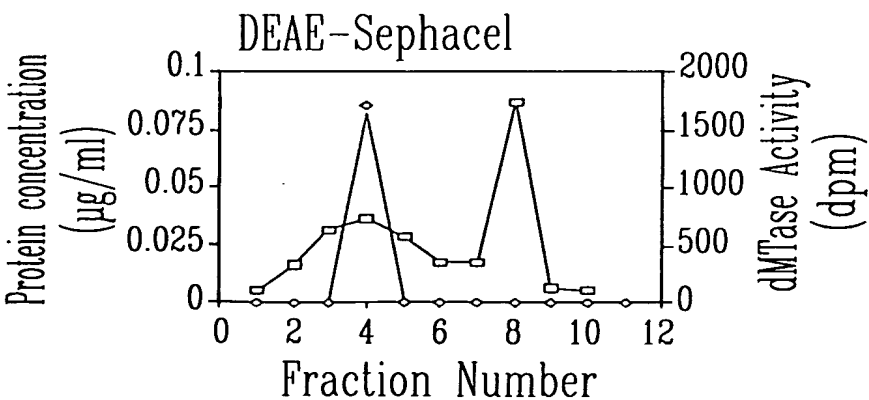
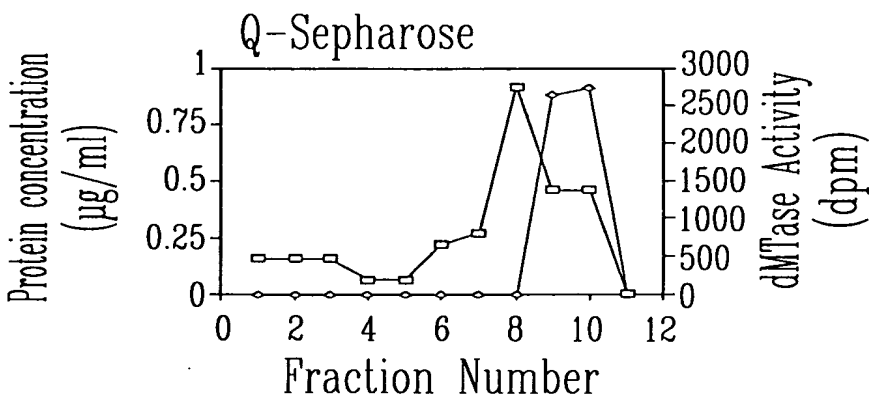
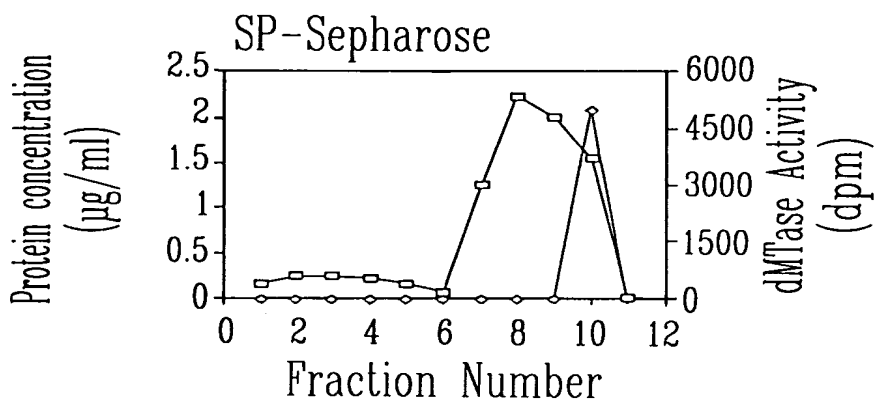
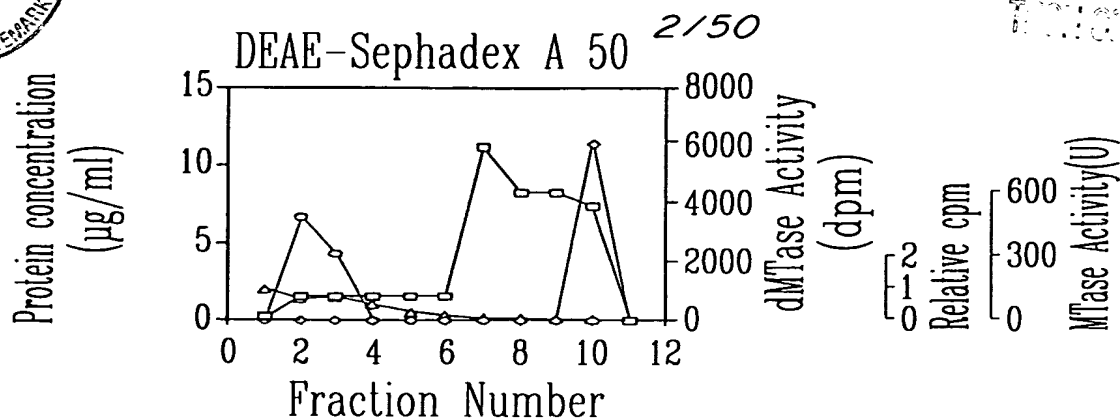


FIG. 1A



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FIG. 1





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3/50

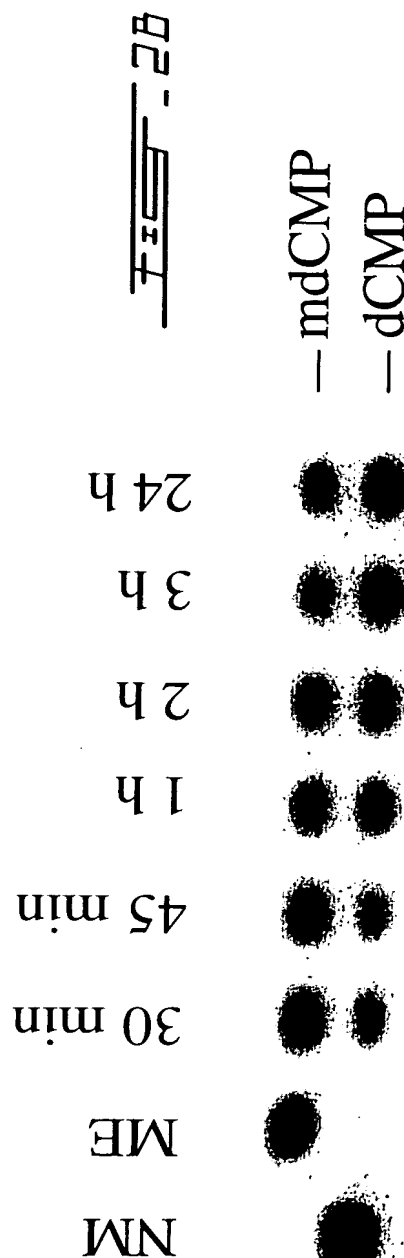
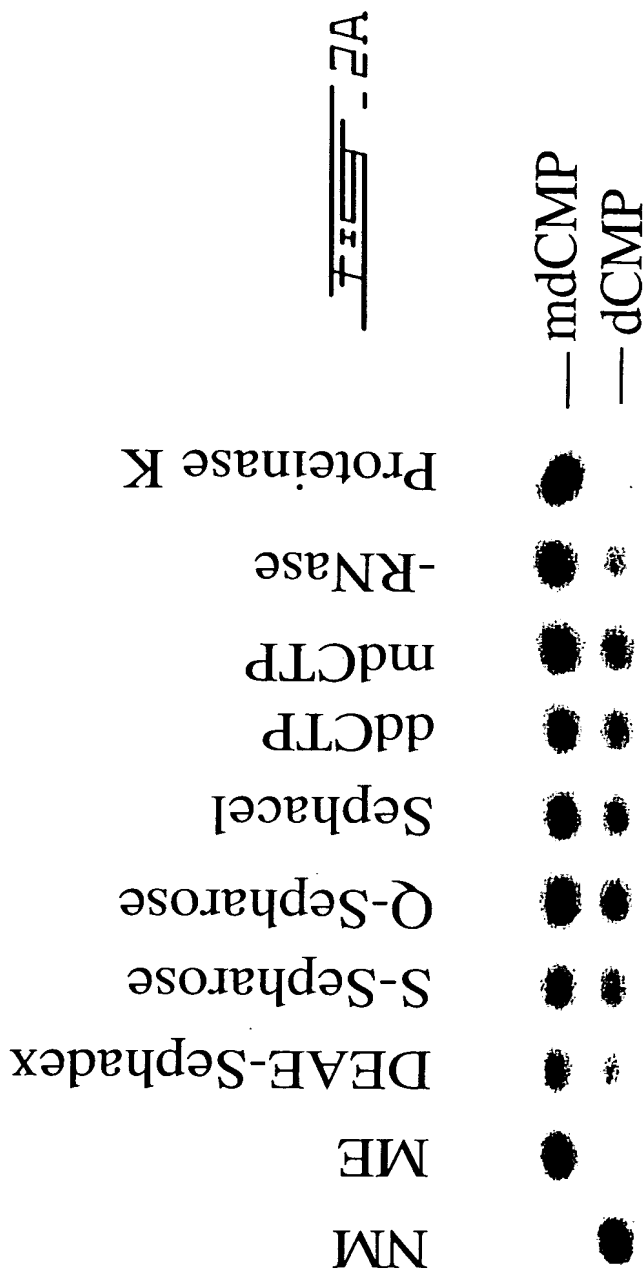




FIGURE 2

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TECHNICAL DATA

4/50

picomole cytosine formed

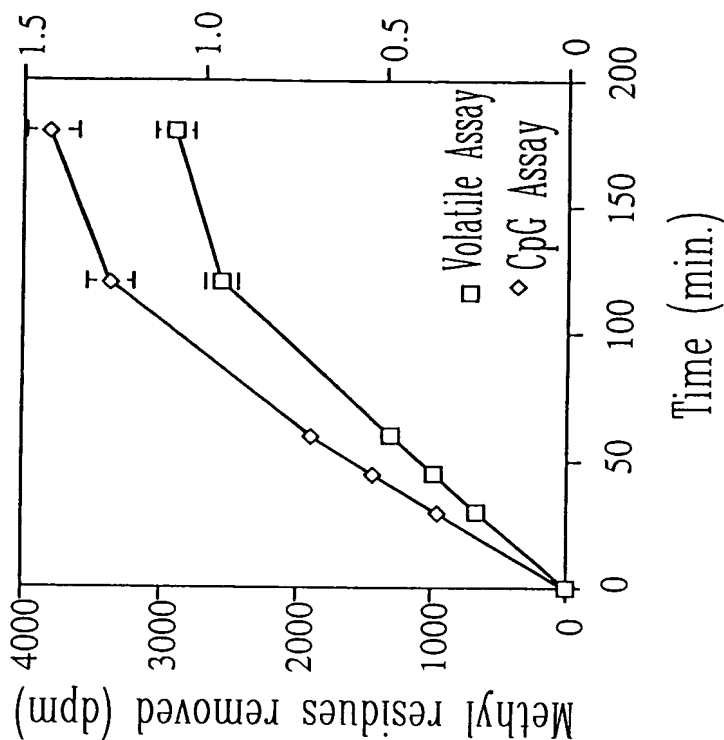


FIGURE 2

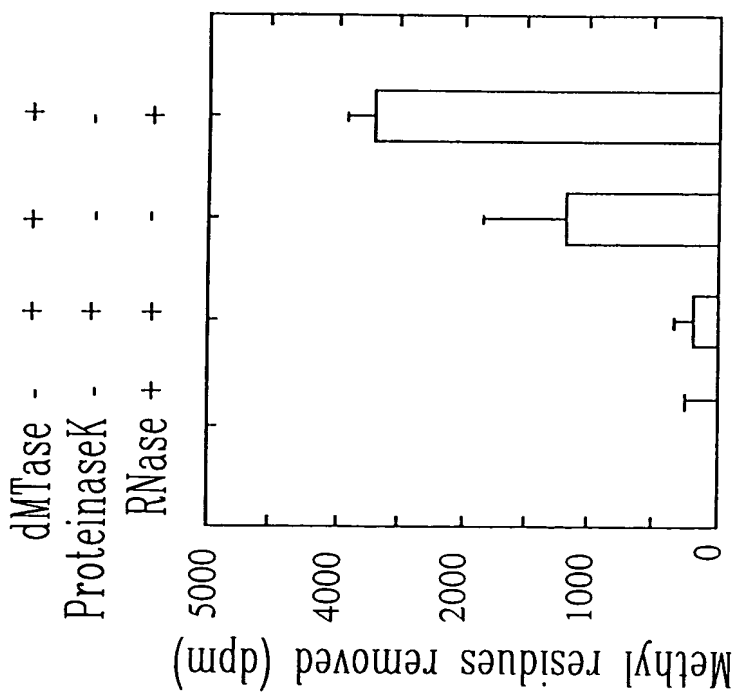


FIGURE 3



SEP 29 2003

5/50

FIG. 3A

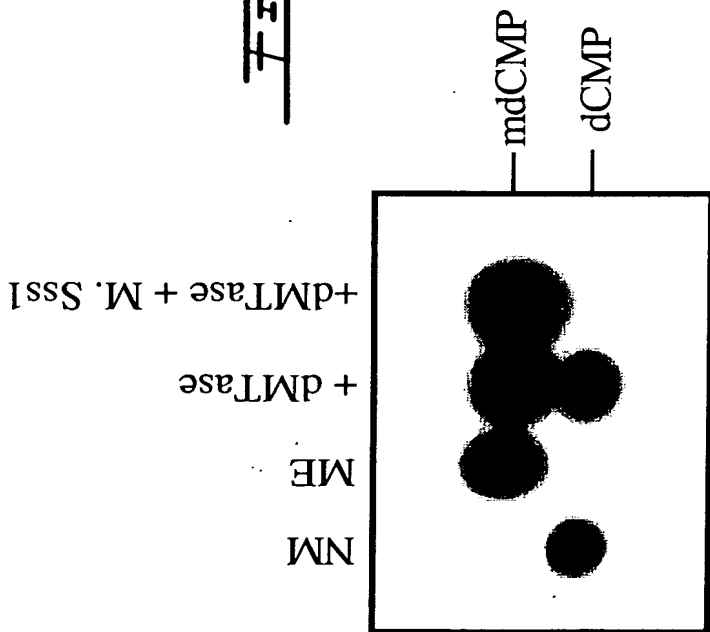
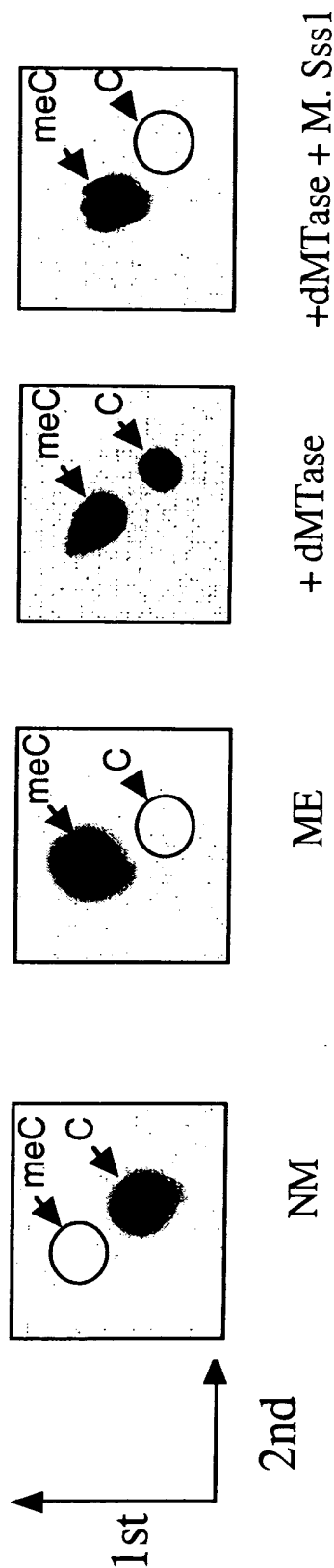


FIG. 3B



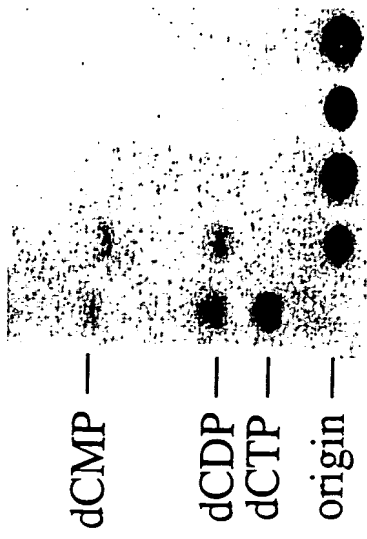


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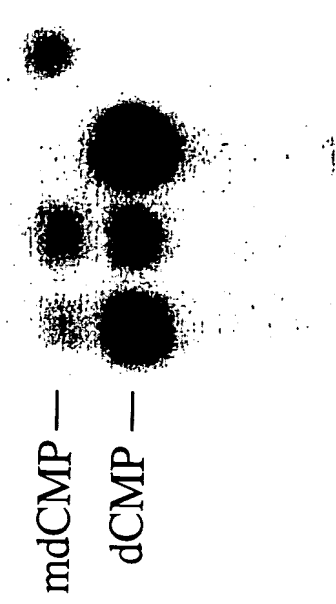
- V PDS

dCTP  
N.E.  
0  
60  
120



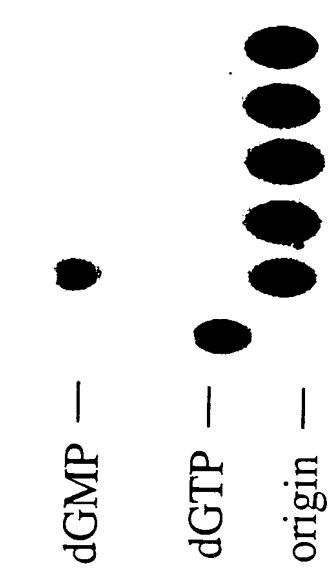
+ V PDS

+RNase  
-RNase  
NM  
ME



- V PDS

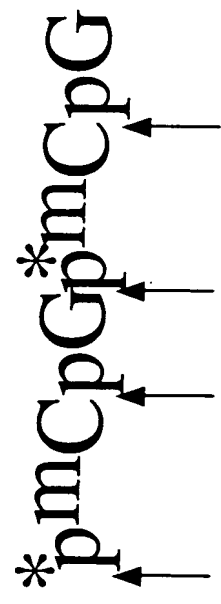
dGTP  
N.E.  
0  
60  
120  
+RNase



6/50

Labeled nucleotide:  
[ $\alpha$ 32P]-dCTP

Labeled nucleotide:  
[ $\alpha$ 32P]-dGTP



FE-3C

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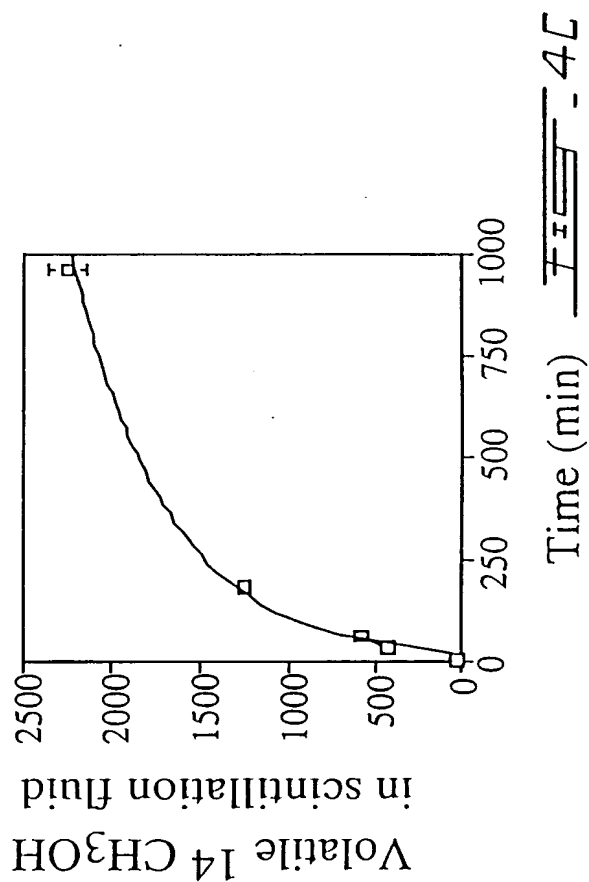
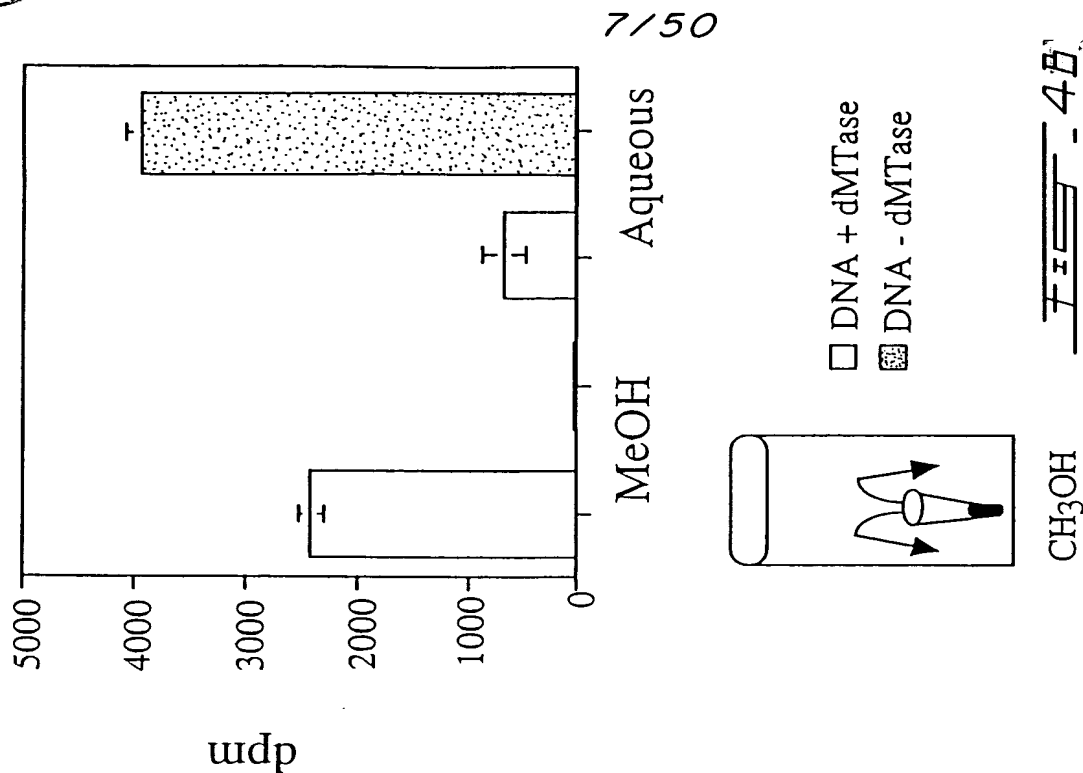
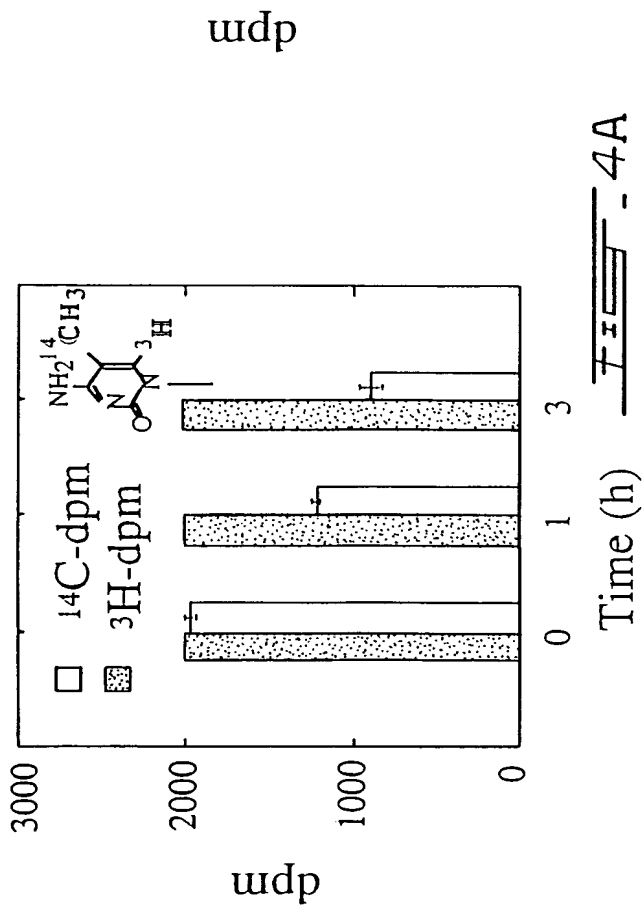




FIG. 10

SEP 29 2003

10/11/2003

8/50

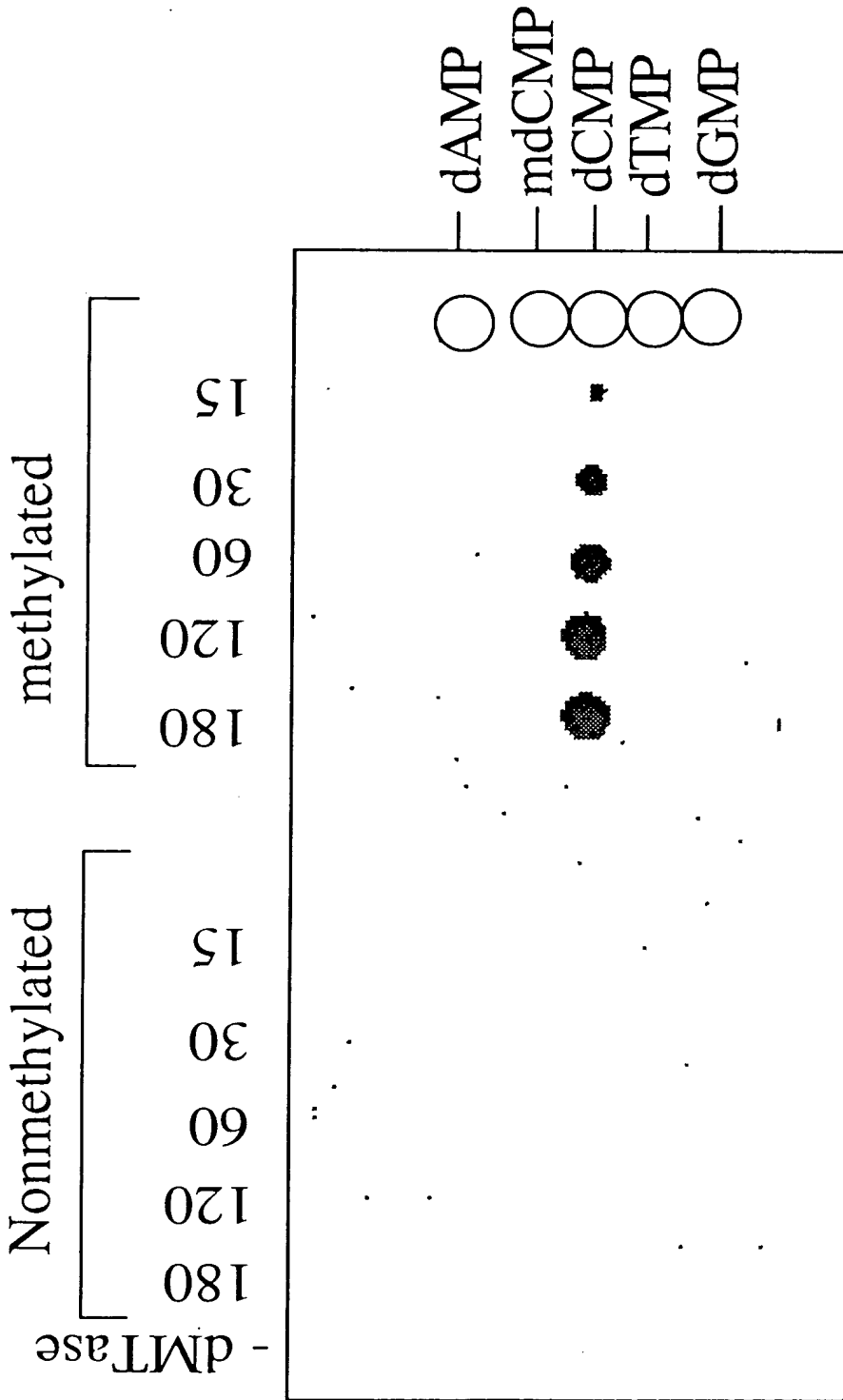


Fig. 10 - 40





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9/50

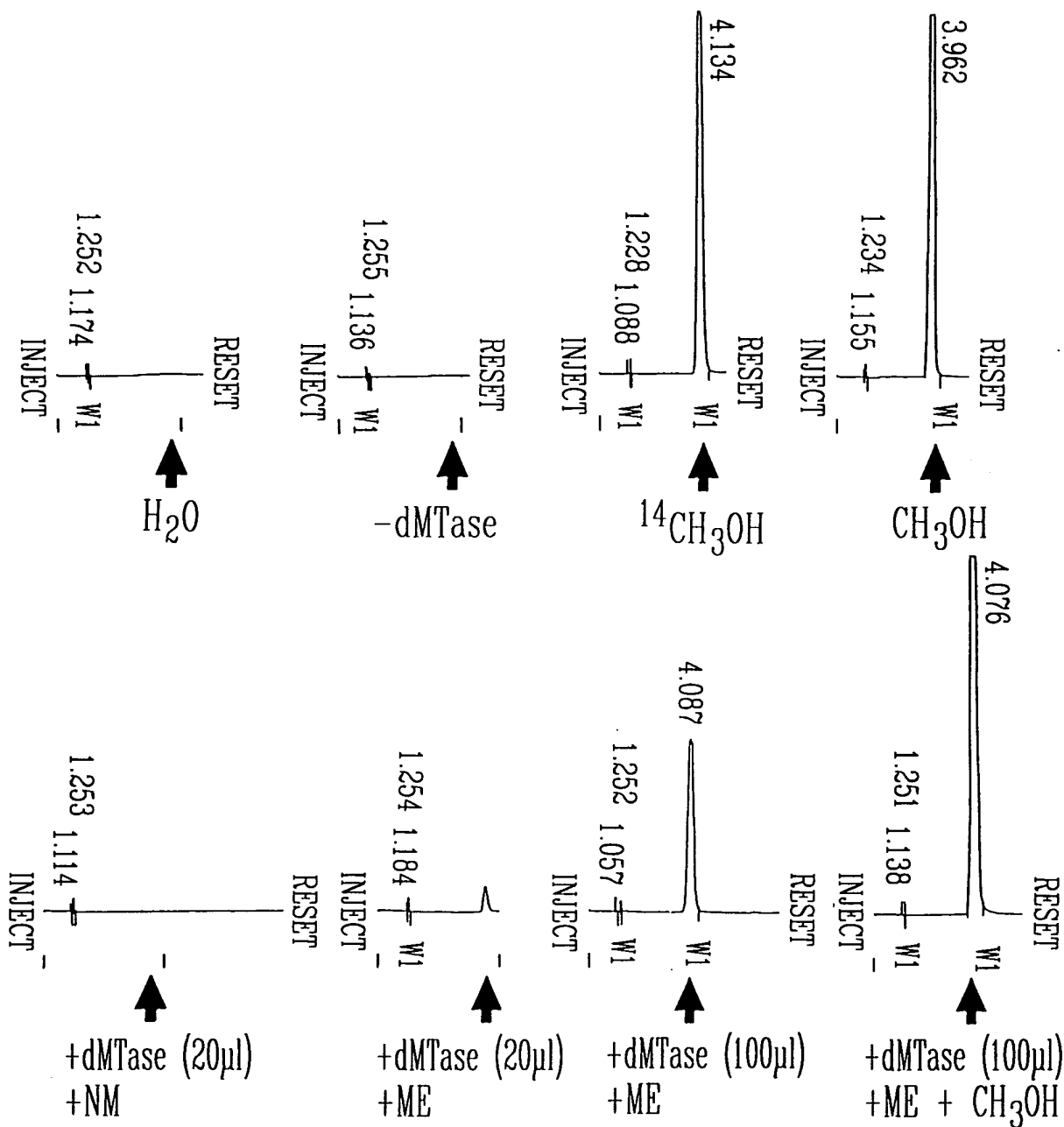
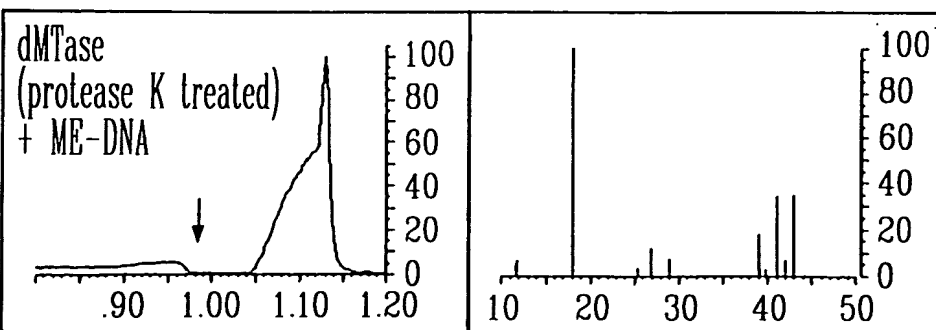
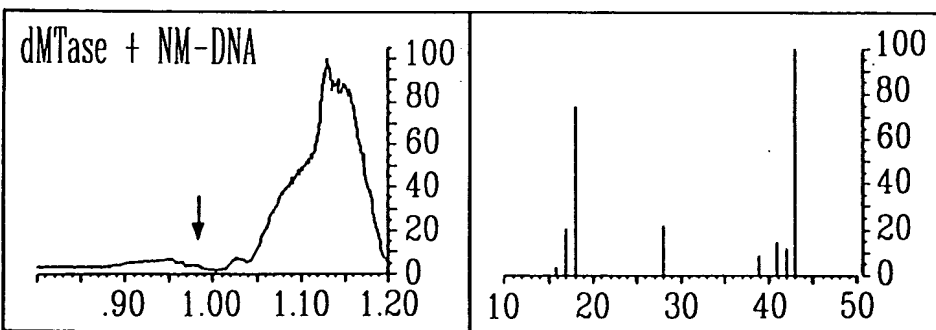
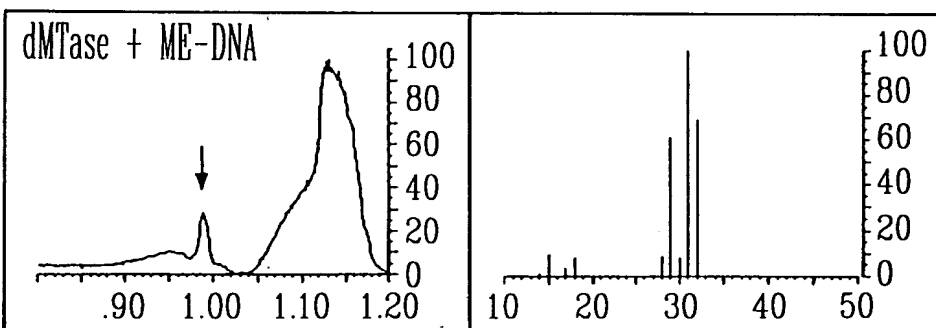
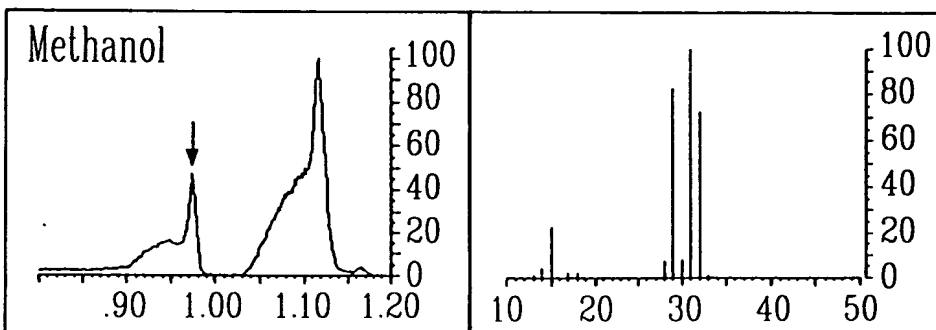
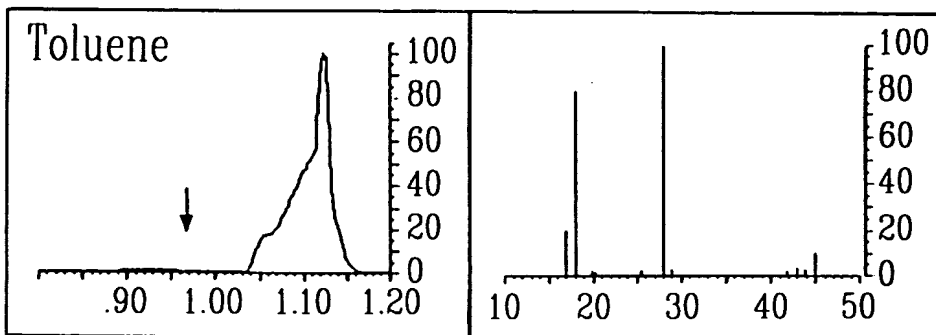


FIG. 4E



10/50

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$$\Delta G_{\text{Reaction}} = (93) - (103 + 91.5) = (-101.5) \text{ Kcal}$$



12/50

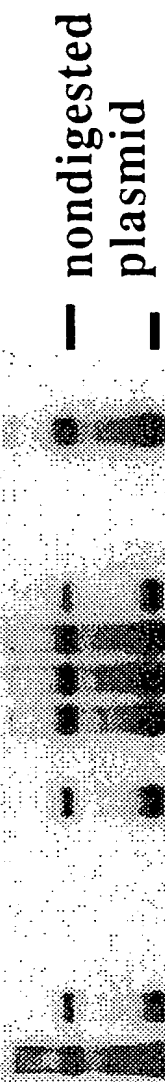
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TECHNICAL UNIT

M.MspI+M.SssI      -      +      +      +

dMTase      -      -      -      +

--	--	--	--	--

EcoRII	+	+	+	+
DpnI	+	+	+	+
HpaII	+	+	+	+
HhaI	+	+	+	+
MspI	+	+	+	+



- nondigested  
- plasmid

- 1.00

- 0.71  
= 0.49  
- 0.32  
- 0.24  
- 0.15

0.45 0.57  
0.40 >  
0.39 0.27  
0.34 0.10  
0.33

FEES - BA

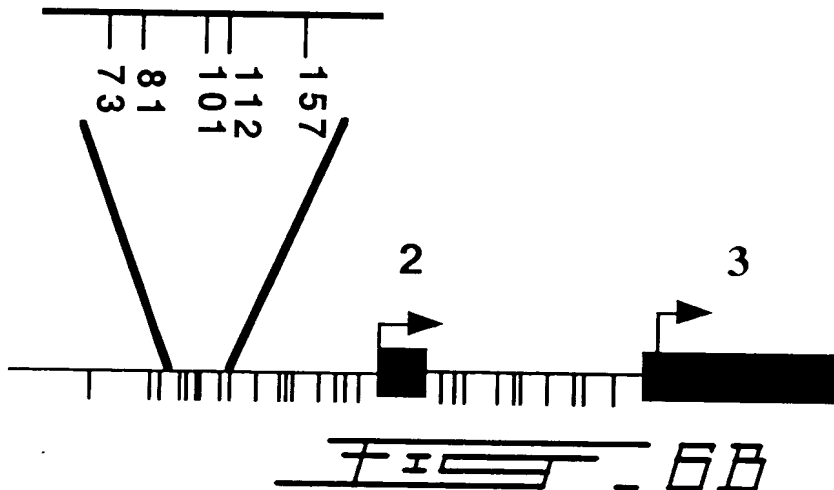
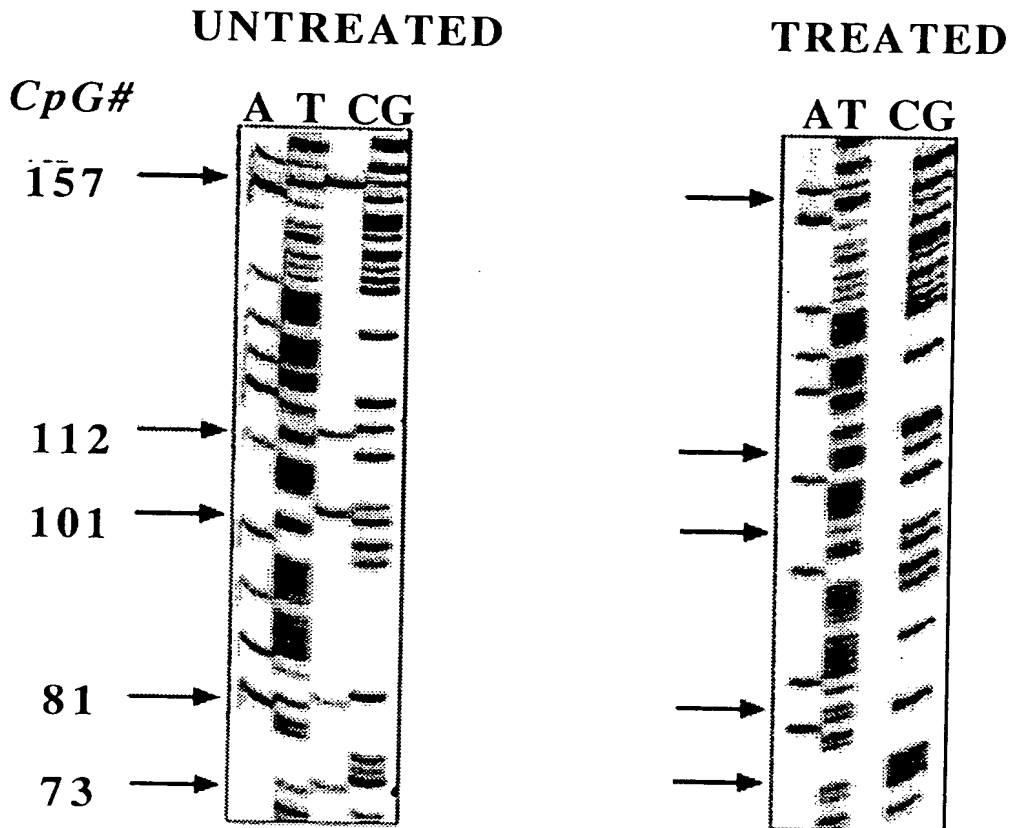


13/50

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14/50

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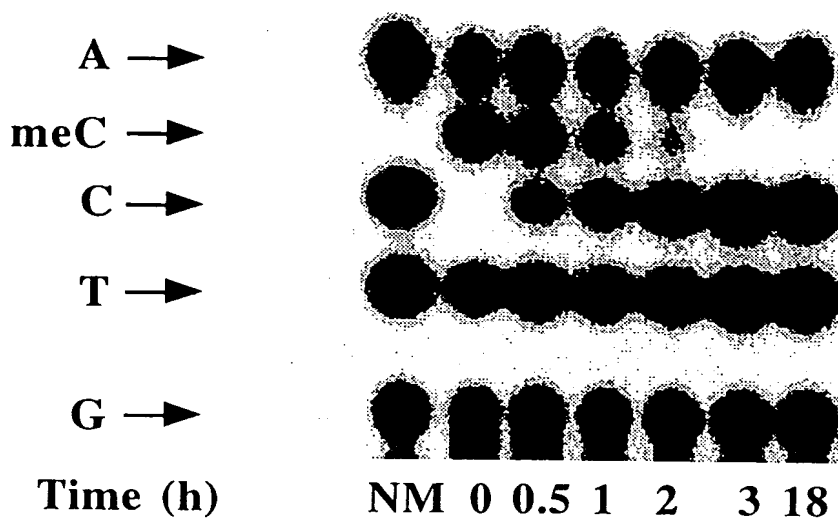


FIG. 1 - 6C

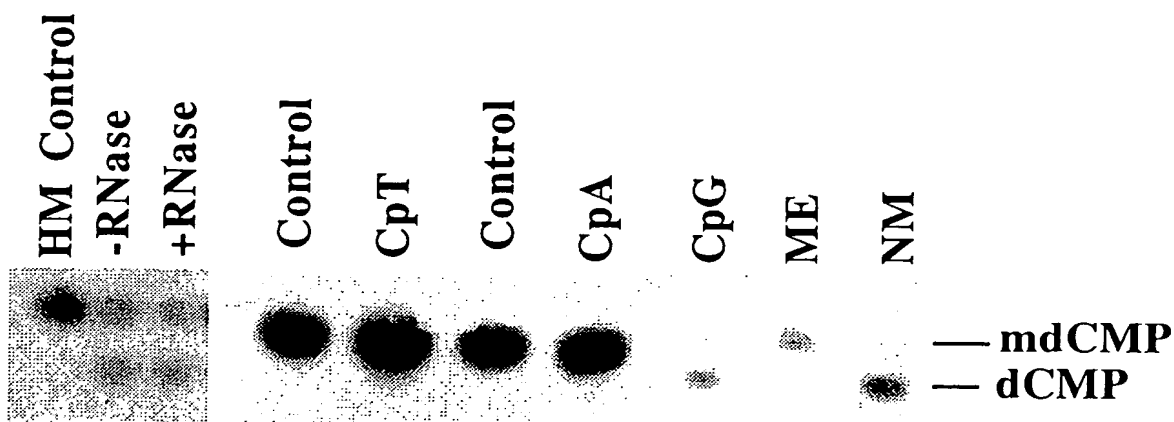
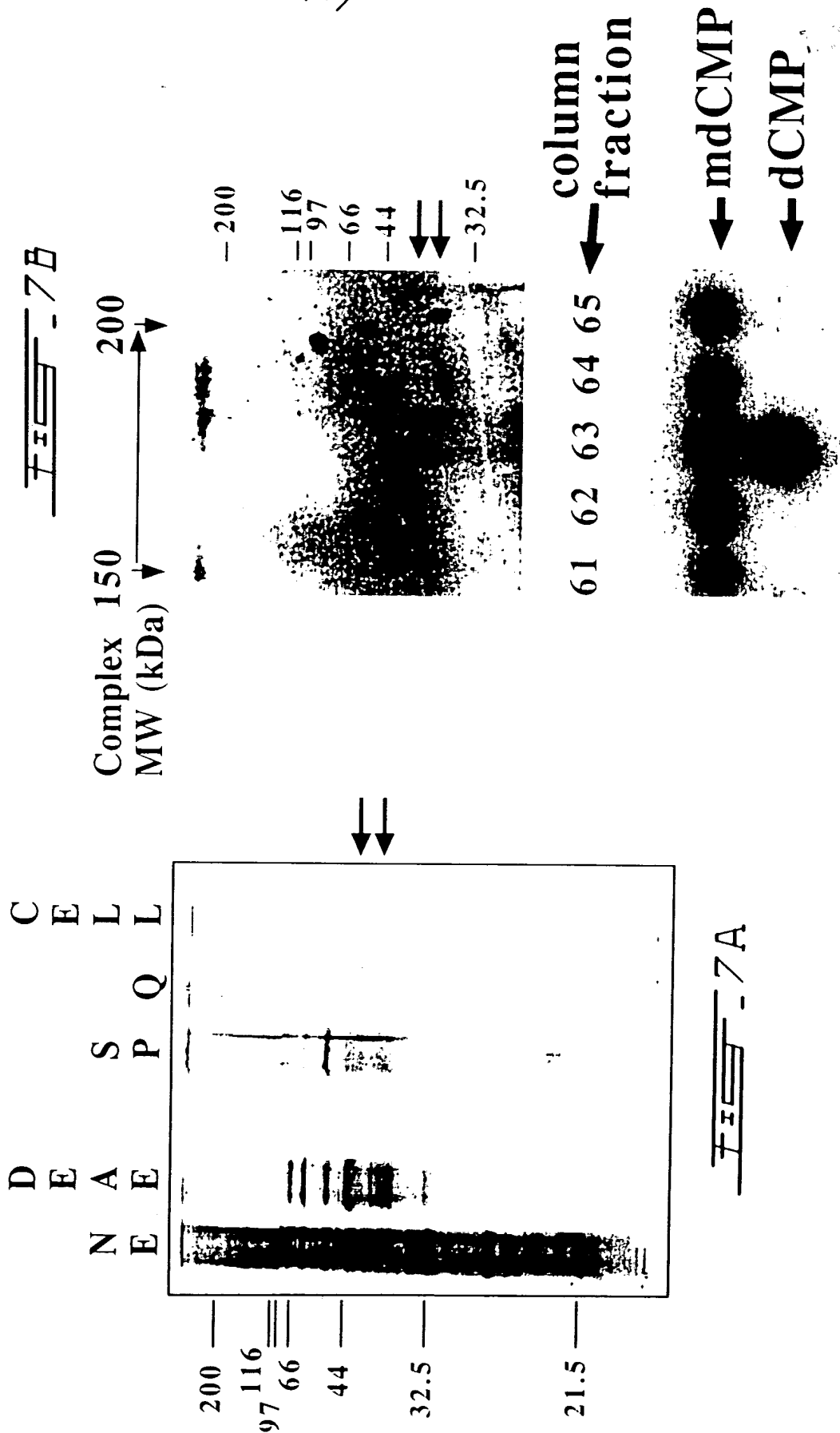


FIG. 2 - 6D



SEP 29 2003

15/50





SEP 29 2003

16/50

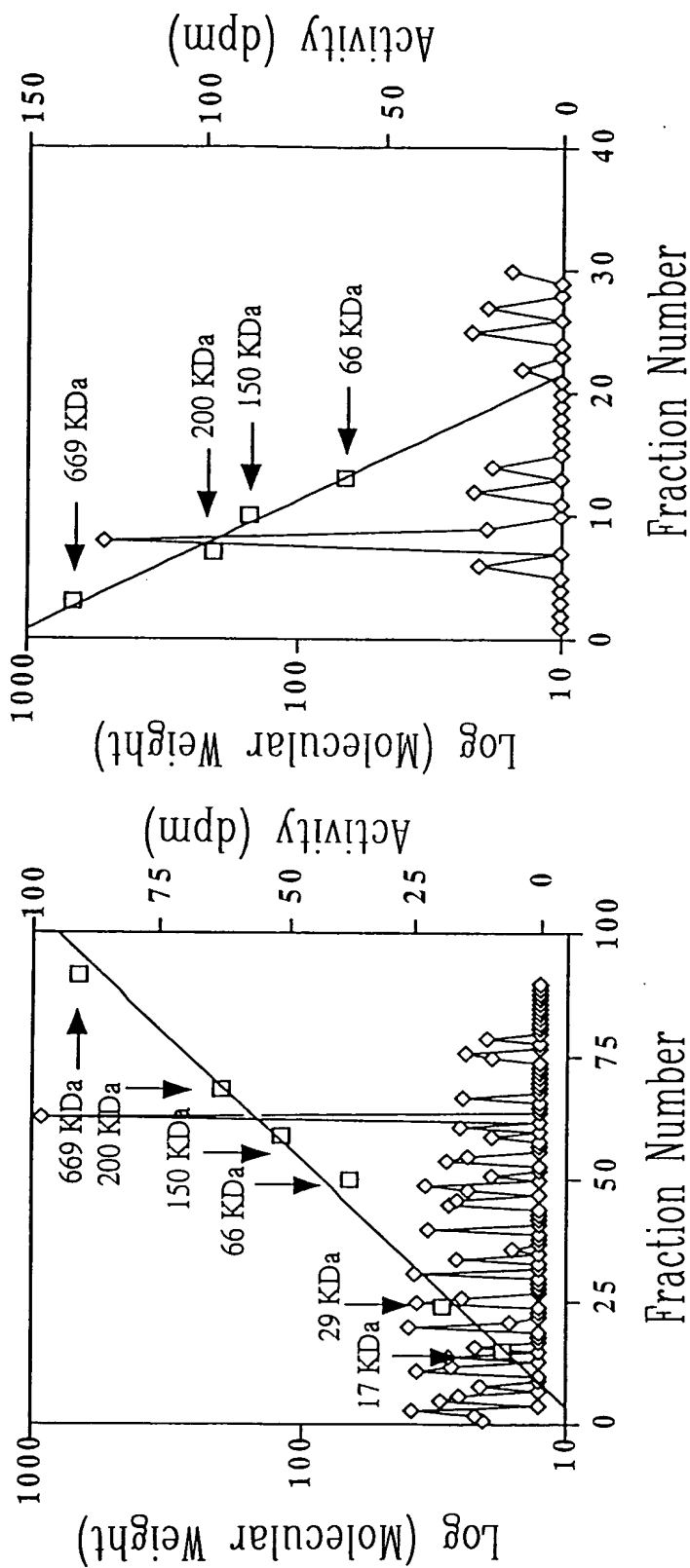


Fig - 7D

Fig - 7C







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18/50

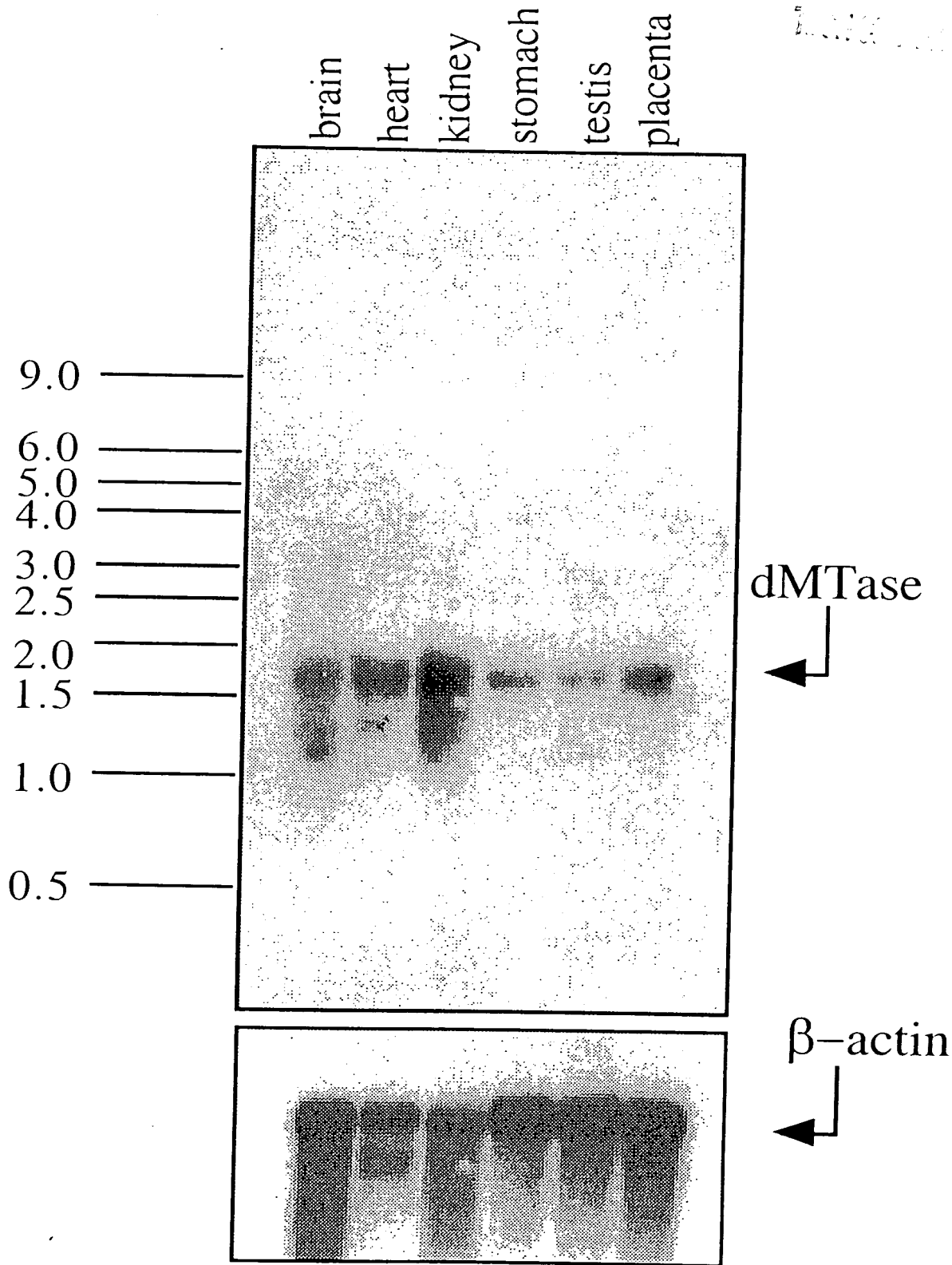


FIG. 8C



SEP 22 2003

# Human DNA demethylase cDNA-dMTase1 and predicted amino acid sequence

5' gggggcgtgg ccccgagaag gcggagacaa gatggccgcc catagcgctt ggaggaccta  
agagggcgtg gccggggcca cggccgggc aggagggccg ctctgtgcgc gcccgctcta  
tgatgcttgc gcgcgtcccc cgcgcgccgc gctgcgggcg gggcgggtct ccgggattcc  
aagggtctcg ttacggaaga agcgcagcg cggctgggga gggggctgga tgcgcgcgca  
cccggggga ggcgcgtgct gcccgagca gagagtgccg cgggcggcag  
cggcgtggc ggcgactccg ccatagaca ggggggccag gccagcgcgc tcgcccctc  
cccgtgagc ggcgtgcgca ggaaggcgc tcggggccgc gccgtggcc gggggcggtg  
gaagcaggcg gccggggcg gcggcgtctg tggccgtggc cggggccggg gccgtggccg  
gggacgggga cggggccggg gccggggccg cggcgtccc ccgagtgccg gcagcggcct  
tggcggcgac ggcggcggct gcggcgccg cggcagcggc ggcggcggcg ccccccggcg  
ggagccggtc ccttcccgt cggggagcgc ggggcgggg gccaggggac cccggggccac  
ggagagcggg aagaggatgg atggccggc cctcccccc ggatggaga aggaggaagt  
gatccgaaaa tctgggctaa gtgctggcaa gagcgatgtc tactactca gtccaagtgg  
taagaagtcc agaagcaagc ctcagttggc aaggtacctg ggaaatactg ttgatctcag  
cagttttgac ttcagaactg gaaagatgat gcctagtaaa ttacagaaga acaaacagag  
actgcgaaac gatcctctca atcaaaataa gggtaaacca gacttgaata caacattgcc  
aattagacaa acagcatcaa ttttcaaca accggtaacc aaagtcacaa atcatcctag

19/50

FIG. 1 - 9A



SEP 22 2003

20/50

taataaagtg aaatcagacc cacaacgaat gaatgaacag ccacgtcagc ttttctggga  
gaagaggcta caaggactta gtgcatcaga tgtaacagaa caaattataa aaaccatgga  
actaccctaa ggtcttcaag ggttgggtcc aggtagcaat gatgagaccc ttttatctgc  
tgttgccagt gctttgcaca caagctctgc gccaatcaca gggcaagtct ccgctgctgt  
ggaaaagaac cctgctgttt ggcttaacac atctcaacc ctctgcaaa cttttattgt  
cacagatgaa gacatcagga aacaggaaga gcgagtacag caagtacgca agaaattgga  
agaagcactg atggcagaca tctgtcgcg agctgctgat acagaagaga tggatatgga  
aatggacagt ggagatgaag cctaagaata tgatcaggta acttctgacc gactttcccc  
aagrgaaaat tcctagaaat tgaacaaaaa tgtttccact ggcttttgcc tgtaagaaaa  
aaaatgtacc cgagcacata gagcttttta atagcactaa ccaatgcctt ttagatgta  
tttttgatgt atatatctat tattcaaaaa atcatgttta ttttgagtcc taggacttaa  
aatagtctt ttgtaatatc aagcaggacc ctaagatgaa gctgagcttt tgatgccagg  
tgcaatctac tggaaatgta gacttacgt aaacatttg tttccccac agttttaata  
agaacagatc aggaattcta aataaatctc ccagttaaag attattgtga cttcactgta  
tataaacata tttttatact ttattgaaag gggacacctg tacattcttc catcatcact  
gtaaaagacaa ataaatgatt atattcacia aaaaaaaa 3'

SEQ ID NO:1

FIG. 1



21/50

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MRAHPGGRCCEEGESAAGSGAGGDS AIEQGGQSALAPSPVSGVR  
REGARGGRGRWKQAGRGVCGRGRGRGRGRGRGRGRGRPPSG  
GSGLGDDGGCGGGGAPRRPVPFPGSAGPPRGP RATESGKRM  
DCPALPPGWKKEEVIKSGLSAGKSDVYFSPSGKKFRSKPQLARYLGNT  
VDLSSFDFRTGKMMPSKLQKNKQRLRNDPLNQNKGPDLNTTLPIRQTAS  
IFKQPVTKVTNHPSNKVKSDPQRMNEQPRQLFWEKRLQGLSASDVTEQII  
KTMELPKGLQGVGPGSNDETLLSAVASALHTSSAPITGQVSAAVEKNPAV  
WLNTSQPLCKAFIVTDEDIRKQEEERVQQVRKKLEALMADILSRAADTEE  
MDIEMDSGDEA

SEQ ID NO: 2

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SEP 29 2003

# Human DNA demethylase homologue-dMTase2 and predicted amino acid sequence

22/50

5' agcgggccga ggagccgggc gcaatggagc ggaagaggtg ggagtgcccg gcgctccccg  
agggctggga gagggagaa gtgcccagaa ggtcggggct gtcggccggc cacagggatg  
tctttacta tagccgagc gggaagaagt tccgcagcaa gccgcagctg gcgcgctacc  
tgggcggctc catggacctg agcaccttcg acttcgcac gggcaagatg ctgatgagca  
agatgaacaa gagccgccag cgcgtgcgt acgactctc caaccaggtc aagggaagc  
ccgacctgaa cacggcgctg cccgtgcgc agacggcgtc catcttcaag cagccggtga  
ccaagattac caaccaccc agcaacaagg tcaagagcga cccgcagaag gcggtggacc  
agccgcgcca gctcttctgg gagaagaagc tgagcggcct gaacgcctc gacattgctg  
aggagctggt caagaccatg gacctccca agggcctgca ggggtggga cctggctgca  
cggatgagac gctgctgtcg gccatcgca gcgccctgca cactagcacc atgcccata  
cgggacagct ctggccgccc gtggagaaga acccggcgt atggctcaac accacgcagc  
ccctgtgcaa agccttcatg gtgaccgacg aggacatcag gaagcaggaa gagctggtgc  
agcaggtgctg gaagcggctg gaggagcgc tgatggcga catgctggcg cacgtggagg  
agctggcccg tgacggggag gcgcgctgg acaaggcctg cgctgaggac gacgacgagg  
aagacgagga ggaggaggag gaggagccc gaggagccc accggacc ggagatggag cacgtctagg  
gcagagggcc tgccgagagc ccgtgctgcc cctggagcc gcctgcagac gcggtcctcg  
gcccacgtg aaccaggctc ggcggcgaag ccagccttg gagacacca ggaggaaagg  
cgtgctcctg gctccctcct cggcccgctc cacttccc ggccctcggg gcacacagct  
ggggctgccc ccacccgaaa gaccctccac gctcgtcctc tacagagtcc ggctcggga  
agtgcggggt gctcctgggc cctgcctggc tccctacgac ctttgggctc gagggcagct

725-90



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23/50

cctccccatg cccgctgtcc cagtccttg agactggaga gcagccagca ggtgccccgc  
agctcggcgc cacggcttgc tgacagctgg gaggtttct cggtctggag gcgtagtttt  
gaaactcaca tcaccactg tgcagcgtga ggacgggact ctggtctgct gtggggggca  
tgcaggacgg cgccactctc tgccctgcca tgcggctggt ggtgccacag agcctcacgg  
tgcctgagtg gcgtgccag ggaggccgct ctcttcagt aaatgtaaca cagtcgaggg  
acgtcatcgg gcagccttcc ctgtgtgcca acgccagcct tcgcttctga aaaccaaact  
ccagccgctg ccagtcggga ctgtgtcgcc cggcgtgccc agaattgctcc actgccagcc  
ggccccctg cctcgggttc cttctgttt agtggcgaca caggcaccca gctttgggg  
ggtgctgacg ctcccagggg tgccaggagc cactgggaca ggttgaggct ccagacgct  
cctcgaggtg ccagctctc cagggagctt ctggcccaag gcttcttga gggatctgct  
ccttaacccc ccagtgcctt ggcgagggca ggttccaagc cacagacgcc tgccccgagt  
ggactttgcg gccagtccct ggggtgcctc ctgggccctg cttggccagt gagggttcct  
aacgggtggg ttcawtggcc tggcccvagc gagccccac ctgcattgac cttagggcca  
tagagagggc ctgtcccggg gctgccccag ccaaggatct ggtcgtgcc ccagggggac  
tgatggggcaa gagtgcgcc tgtggctgga ctgtgacct cctgatggg gcctgaccgc  
gggagctgag gaagcgcgc tccaccgtct gccctccaag gacccgcatg gaggcagtgg  
gctggcagct tcctgctgct ccctgtcaga gtcaaaagcac aaatcctcag gacgggctca  
agggccaggg cagccgaggg aagctccagg tggggaccac gtcttctga ggttggtgcc  
cactggctgg gaccctttgc agtgggggtg cctccccctc gtctgcctgg tggaggggagc  
cgtgggctg gggacgtgac tgaataaagc caccatgggt gg 3'

SEQ ID NO:3

FIG. 1 - SE



Serial No. 09/554,414  
REPLACEMENT SHEET

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24/50

MERKRWECPALPQGWEREVPRRSGLSAGHRDVFYSPSGKKFRSKPQLA  
RYLGGSMDLSTFDFTGKMLMSKMNKSRQVRVYDSSNQVKGKPDNLNTALP  
VRQTASIFKQPVTKITNHPSNKVKSDPQKAVDQPRQLFWEKKLSGLNAFD  
IAEELVKTMDLPKGLQGVGPGCTDETLLSAIAASALHTSTMPITGQLSAAV  
EKNPGVWLNTTQPLCKAFMVTDEDIRKQEEELVQQVRKRLEEALMADMLAH  
VEELARDGEAPLDKACAEDDDDEDEEEEEPPDPPEMEHV

SEQ ID NO: 4

7-11-9F





SEP 29 2003

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>411)		Seq2(1>291)		Similarity		Gap		Consensus	
human dMTase1 protein	human dMTase2 protein	human dMTase1 protein	human dMTase2 protein	Index	Index	Number	Length	Length	Length
(148>397)	(4>253)	(148>397)	(4>253)	76.0	76.0	0	0	250	250
(148>397)	(4>253)	(148>397)	(4>253)	76.0	76.0	0	0	250	250
v150	v160	v170	v180	v190	v200	v210			
KRMDCPALPPGWKKEEVIRKSGLSAGKSDVYFSPSGKKFRSKPQLARYLGNIVDLSSFDFTGKMMPSK									
KR :CPALP.GW.:EEV R:SGLSAG..DV:Y:SPSGKKFRSKPQLARYLG.:DLS:FDFTGKM: SK									
KRWECPALPQGWEREFEVPRRSGLSAGHRDVFYSPSGKKFRSKPQLARYLGGMDLSTFDFTGKMILMSK									
25/50									
^10 ^20 ^30 ^40 ^50 ^60 ^70									

v220 v230 v240 v250 v260 v270 v280  
LQKNKQRLRNDPLNQKGPDLNTILPIRQTASIFKQPVTKVINHPNKNVKSQDPQRMNEQPRQLFWEKRL  
::K::QR:R D: NQ KGKPDINT:LP:RQTASIFKQPVTK:TNHPNKNVKSQDPQ: :QPRQLFWEK:L  
MNKSRQVRVYDSSNQKGPDLNTALPVRQTASIFKQPVTKITINHPNKNVKSQDPQKAVDQPRQLFWEKRL  
^80 ^90 ^100 ^110 ^120 ^130 ^140

FEI-96



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26/50

v290	v300	v310	v320	v330	v340	v350
QGLSADVTEQIIKIMELPKGLQGVGPGSNDIEILLSAVASALHTSSAPITGQVSAAVEKNPAAWLNTSQP						
GL:A D::E:::KIM:LPKGLQGVGPG..DEIILSA:ASALHTS: PITGQ:SAAVEKNP:VWLNT:QP						
SGLNAFDIAEELVKIMDLPKGLQGVGPGCTDEIILSAIASALHTSIMPITGQLSAAVEKNPVGWLNTITQP						
^150	^160	^170	^180	^190	^200	^210
v360	v370	v380	v390			
LCKAFIVTDEDIRKQEEERVQQVRKLEEFALMADILSRAAD						
LCKAF:VIDEDIRKQEE VQQVRK:LEEFALMAD:L::::						
LCKAFMVIDEDIRKQEEELVQQVRKLEEFALMADMLAHVEE						
^220	^230	^240	^250			



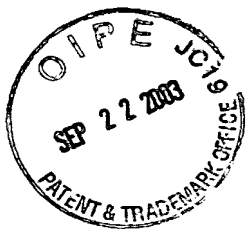
SEP 20 2003

# Mouse DNA demethylase-dMTase1 and predicted amino acid sequence

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gagccggctg gggagggggc tggatgcgcg cgcacccggg gggaggccgc tgctgcccgg  
agcaggagga gggggagagc gcggcgggcg gcagcggcgc tggcggcgac tccgccatag  
agcagggggg ccagggcagc gcgctcgctc cgtccccggt gagcggcgtg cgcagggaag  
gcgctcgggg cggcgcccggt ggcggggggc ggtggaagca ggcggcccgg ggcggcgggc  
tctgtggcgg tggccgtggc cgtggccggg gtccggggcg tggcggggc cggggccggg  
gccgcggcgg tcccagagt ggcggcagc ggcggcagc gccttggcgg cgcggcggc ggcggcgcg  
gcggctgcgg cgtcggcagc ggtggcgggc ggtggcgggc tgcggcccg gcgggacct gtccctttcc  
cgtcggggag ctcggggcgg gggccaggg gacccgggc caggagagc agtgatccga aaatcagggc  
tggactgccc ggccctcccc caaggcggat gtctactact ctgttgacct tagcagtgtt gacttcagga  
aacctcagct ggcaagatac gatgcctagt aaattacaga agaacaagca gagactccgg aatgaccccc  
ccaatcagaa caagggtaaa ccagacctga acacaacatt gccaataga caaactgcat  
caattttcaa gcaaccagta accaaattca cgaaccacc gagcaataag gtgaagtcag  
accccagcg gatgaatgaa caaccacgtc agcttttctg ggagaagagg ctacaaggac  
ttagcgcac agatgtaaca gaacaaatta taaaaccat ggagctacct aaaggtcttc  
aaggagtcgg tccaggtagc aatgacgaga cccttctgtc tgctgtggcc agtgctttac

27/50

FIG. 1



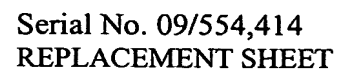
SEP 29 2003

28/50

acacaagctc tgcgcccac acaggacaag tctctgctgc cgtggaaaag aaccctgctg  
tttggcttaa cacatctcaa cccctctgca aagctttcat tgttacagat gaagacatta  
ggaacacagga agagcgagtc caacaagtac gcaagaaact ggaggaggca ctgatggccg  
acatcctgtc ccgggctgag gacacggagg aagtagacat tgacatggac agtggagatg  
aggcgtaaga atatgatcag gtaactttcg actgacctc cccaagagca aattgctaga  
aacagaatta aacatattcc actgggttcc gcctgtaaga aaaagtgtac ctgagcacat  
agctttttaa tagcactaac caatgccttt ttagatgtat ttttgatgta tatacttatt  
attccaaatg atgtttattt tgaatcctag gacttaaaat gactctttta taatagcaag  
cagggccctt ccggtgcagt gcagctttga gcccagggtgc agtctactgg aaaggtagca  
cttacgtgaa atatgtgtt cccccacagt tttaataataa acagatcagg agtaccacaaat  
aagtttccca attaaagatt attatacttc actgtatata aacagatttt tatactttat  
tgaaaagaaga tacctgtaca ttcttccatc atcactgtaa agacaaaataa atgactatat  
tcac 3'

SEQ ID NO:5

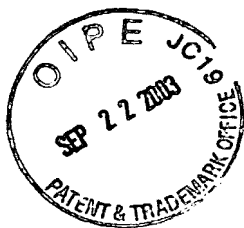
FILED - 9J



SEP 29 2053

SEQ ID NO: 6

FILE OK



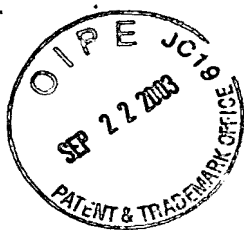
SEP 29 2003

30/50

# Mouse DNA demethylase-dMTase2 and predicted amino acid sequence

5' cacgcgcggg cgggtgggcg gagcgcccc ctagcgggg gctgtgaagc gcgggggaggg  
ggccgagcgg gtggcgaaagc cggcgcgcg cggctgggg gcggaggcg gagggccgtg  
ggacagaaca gctgcggcga gtggcggcgg cggagggagc cgaatcggcg acgagcccgg  
gggtcgcaac ttgcagaagc ggcgcggcgg gcggcatcgg ccacggcggg cggaaaagcc  
ggggcgcaat ggagcggaag aggtgggagt gcccgcgct ccgcaggcg tgggaaaggg  
aagaagtgcc caggaggctg gggctgtcgg ccggccacag ggatgtcttt tactatagcc  
ccagcgggaa gaagtccgc agcaagccac aactggcacg ttacctgggc ggatccatgg  
acctcagcac cttcgacttc cgcaccggaa agatgttgat gaacaagatg aataagagtc  
gccagcgtgt gcgctatgat tcttccaacc aggtcaaggg caagcctgac ctgaacacccg  
cgctgcctgt acggcagact gcattccatct tcaagcaacc ggtgaccaag atcaccaacc  
acccagcaa caaggtcaag agcaccgcg agaaggcagt ggaccagccg aggcagcttt  
tctgggagaa gaagctaagt ggattgagtg cctttgacat tgcagaagaa ctggtcagga  
ccatggactt gcccaaggcg ctgcaggag ctggccctgg tgggtacagat gagacgctgc  
tgtcagccat tgcgagtgt ctacacacca gcaccctgcc cattacaggc cagctctctg  
cagccgtgga gaagaaccct ggtgtgtggc tgaacactgc acagccactg tgcaaaagcct  
tcatggtgac agatgacgac atcaggaagc aggaggagct ggtacagcag gtacggaagc  
gcctggagga ggcactgatg gccgacatgc tagctcatgt ggaggagctt gcccgagacg  
gggaggcacc actggacaag gcctgtgcag aggaggaaga ggaggaggaa gaggaggagg

FIG. 1



SEP 29 2003

31/50

SEQ ID NO:7

FIG. 1

aagagccgga gccagagcga gtgtagcaca ggtgccctgc ccaagtctgg gctgcagact  
gccttcagcc ttgcctggac caggtagggg ccagacctgt aggaggcagc cgtccacctc  
ctttccaaag cctcctgctt ccagggtctca gtgcaggagg cccctgtgga ccttgaactc  
acttgtccct gcgctgcctg gcaggaagcc ccacactgaa agcagatgag cagtgaccca  
actgagaggc cacctggaca cagtcacctc cctgcctcct tatcatagga caaggccttg  
cttggcaccc aggagctggg agccgtgttg ggtgctggag gaagtcttg gaaacacacc  
tggctatgcc caccttatgt ccctaaggct attacaggcc agggtttggg ctgctccggc  
ccacagggct gccagcctc ccacactga gggtcagcag ccaccaggga agtcacttctc  
cttcaataaa ctgatggtag gaacttggtg 3'



32/50

SEP 20 2003

MERKRWECPALPQGWEREEVPRRSGLSAGHRDVFYSPSGKKFRSKPQLA  
RYLGSMDLSTFDFTGKMLMNKMNKSQRQVRDYDSSNQVKGPDLNTALP  
VRQTASIFKQPVTKI TNHPSNVKSDPQKAVDQPRQLFWKKLSGLSAFD  
IAEELVRTMDLPKGLQGVGPGCTDETLLSAIASALHTSTLPITGQLSAAV  
EKNPGVWLNTAQPLCKAFMVTDDDIRKQEELVQQVRKRLEEEALMADMLAH  
VEELARDGEAPLDKACAEFFFFFFFFEEEEPEPERV

SEQ ID NO: 8

FILED - 9N





SEP 20 2003

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>414)

Seq2(1>285)

mouse dMTase2 protein

Similarity

Gap

Length

Consensus

mouse dMTase1 protein  
(151>400)

(4>253)

Index

Number

Length

Length

(151>400)

(4>253)

75.2

0

0

250

v160

v170

v180

v190

v200

v210

v220

KRMDCPALPPGWKKEEVIRKSGLSAGKSDVYFSPSGKKFRSKPQLARYLGNVAVDLSSDFRTGKMMPSK

KR :CPALP.GW.:EEV R:SGLSAG..DV:Y:SPSGKKFRSKPQLARYLG.:DLS:FDFTGKM: :K

KRWECPALPQGWEREVEVPRRSGLSAGHRDVFYSPSGKKFRSKPQLARYLGGSMDSLSTFDFTGKMLMNK

^10

^20

^30

^40

^50

^60

^70

33/50

v230

v240

v250

v260

v270

v280

v290

LQKNKQRLRNDPLNQNKGKPDNLNITLPIRQTASIFKQPVTKFTNHPSNKVKSDPQRMNEQPRQLFWEKRL

::K::QR:R D: NQ KGKPDNLN:LP:RQTASIFKQPVTK:TNHPSNKVKSDPQ: :QPRQLFWEK:L

MNKSQRQVRDSSNQVGKGPDLNTALFVRQTASIFKQPVTKITNHPSNKVKSDPQKAVDQPRQLFWEKKL

^80

^90

^100

^110

^120

^130

^140

FEI-90



SEP 22 2003

v300 v310 v320 v330 v340 v350 v360  
QGLSASDVTEQIITIMELPKGLQGVGPGSNDITLLSAVASALHTSSAPITIGQVSAAVEKNPAAVWLNITSQP  
GLSA D::E:::TM:LPKGLQGVGPG..DETLLSA:ASALHTS: PITGQ:SAAVEKNP:VWINT:QP  
SGLSAFDIAEELVRIMDLPKGLQGVGPGCITDETLLSAIASALHTSTLPTITGQLSAAVEKNPVGWLNITAQP  
^150 ^160 ^170 ^180 ^190 ^200 ^210

34/50

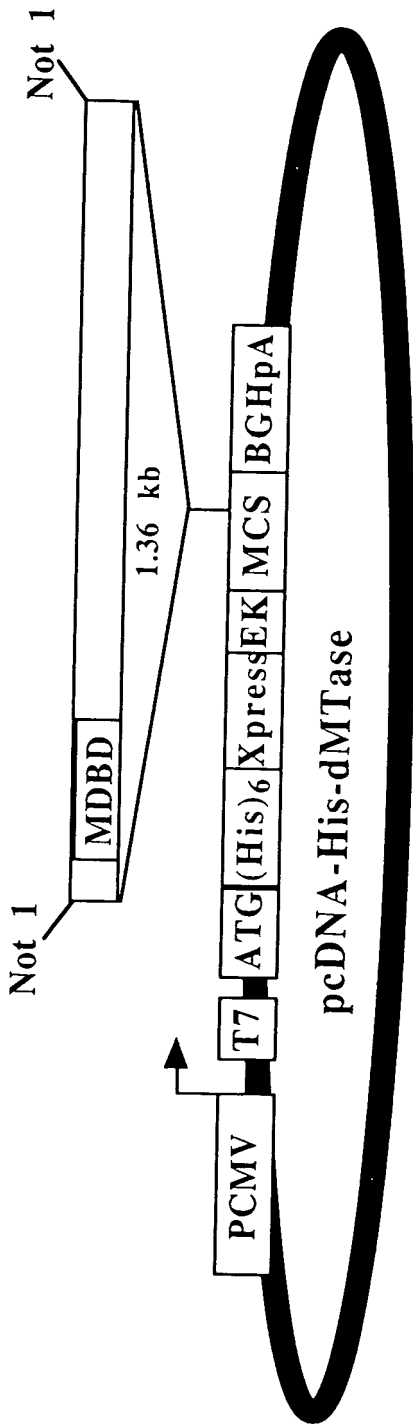
v370 v380 v390 v400  
LCKAFIVTDEDIRKQEEERVQQVRKKLEEFALMADILSRAAD  
LCKAF:VTD:DIRKQEE VQQVRK:LEEFALMAD:L:::  
LCKAFMVTDDDIRKQEEELVQQVRKRLLEEFALMADMLAHVEE  
^220 ^230 ^240 ^250

FILED - 9 P

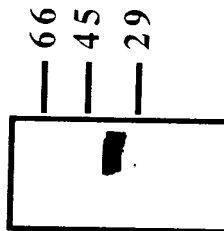


35/50

SEP 20 2003



miframe  
dMTase



Test - 10A



36/50

SEP 29 2003  
PATENT & TRADEMARK OFFICE

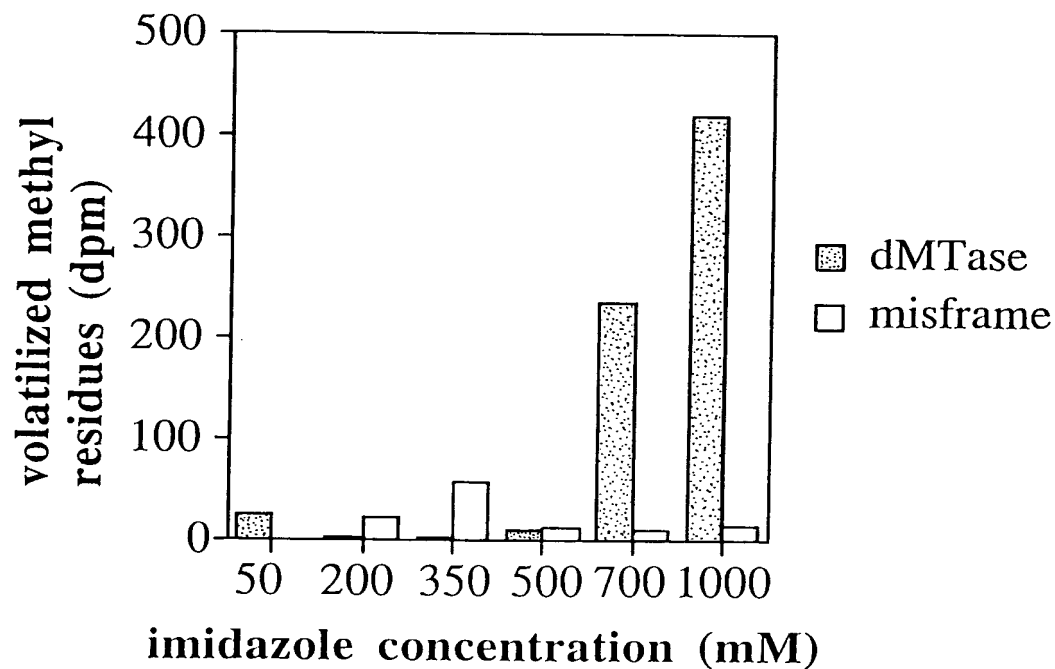
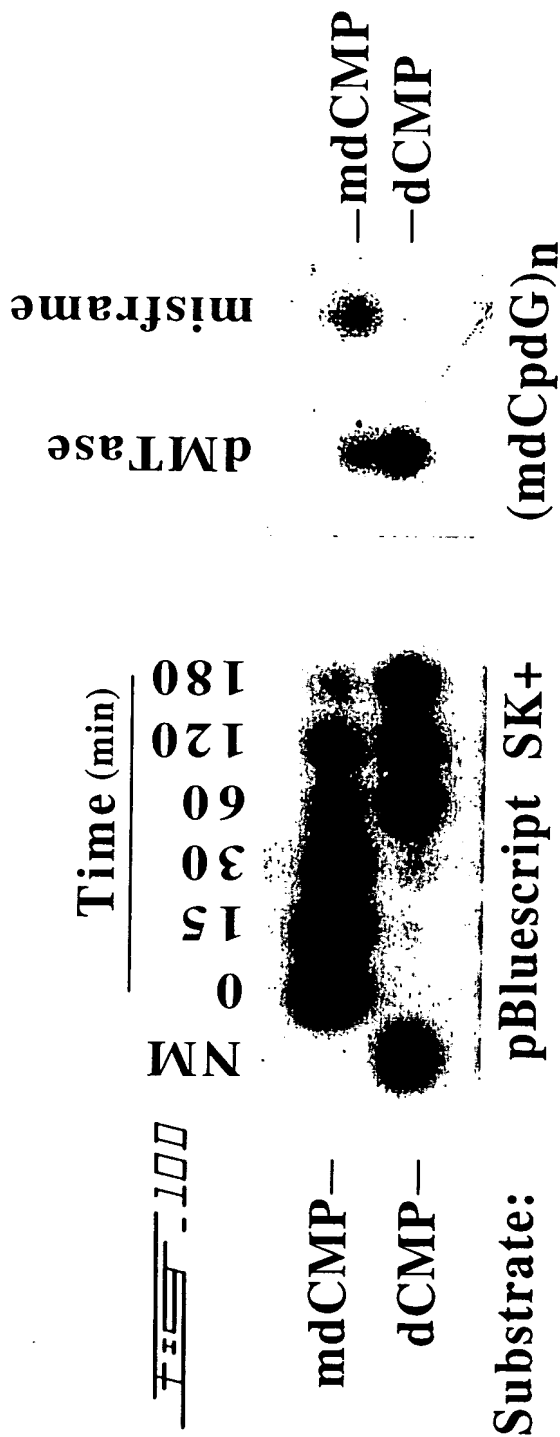
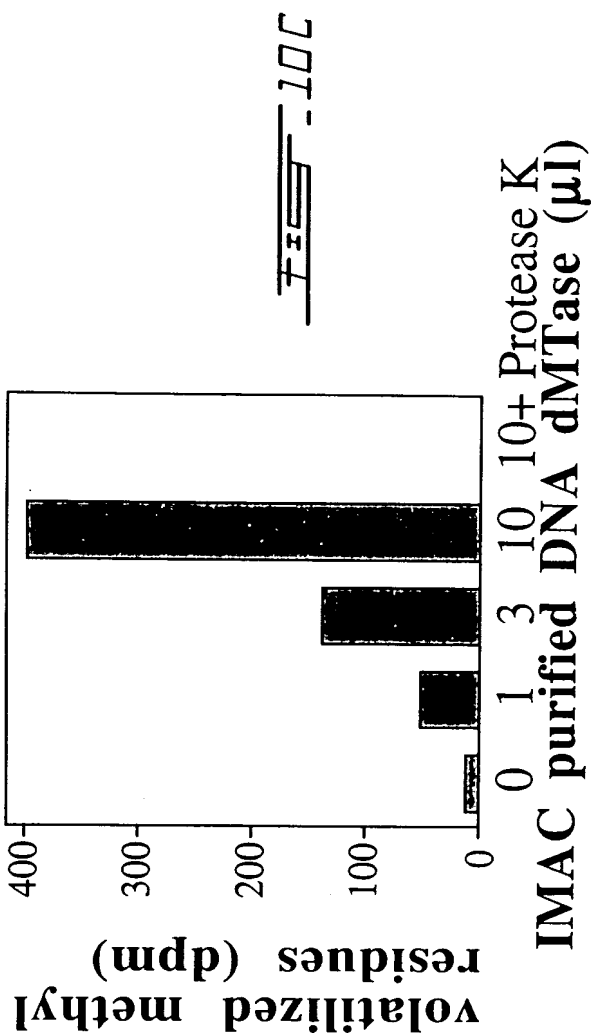


FIG. 10B



37/50

SEP 20 2003





38/50

SEP 29 2003

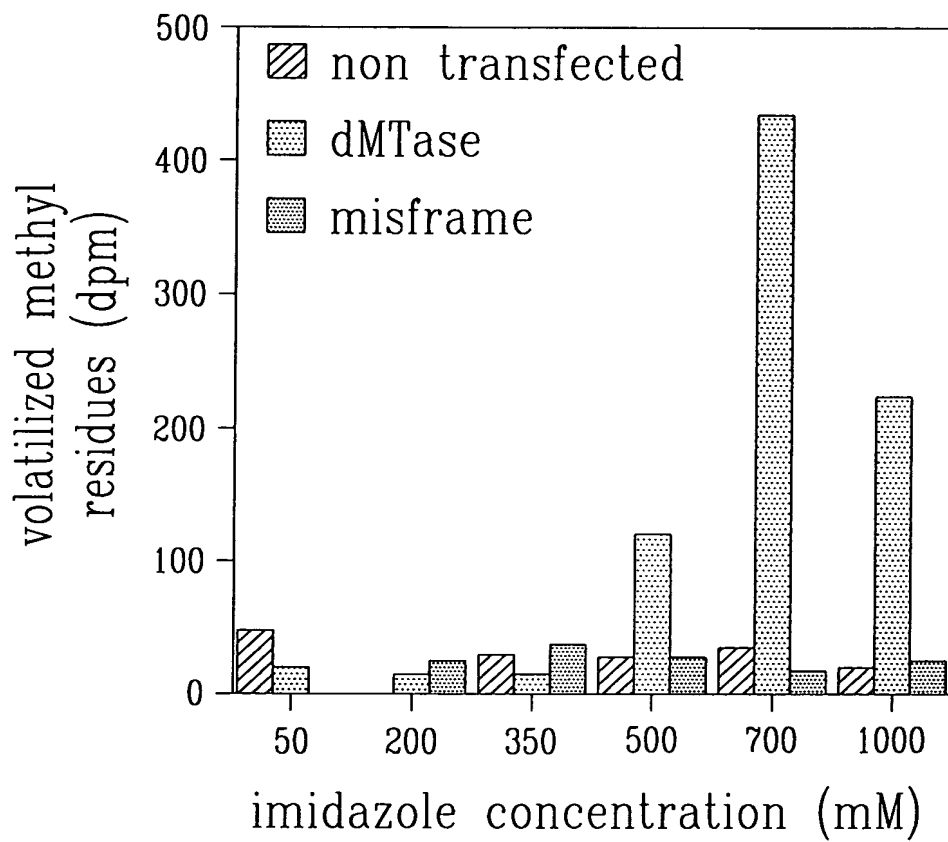
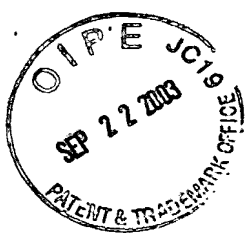
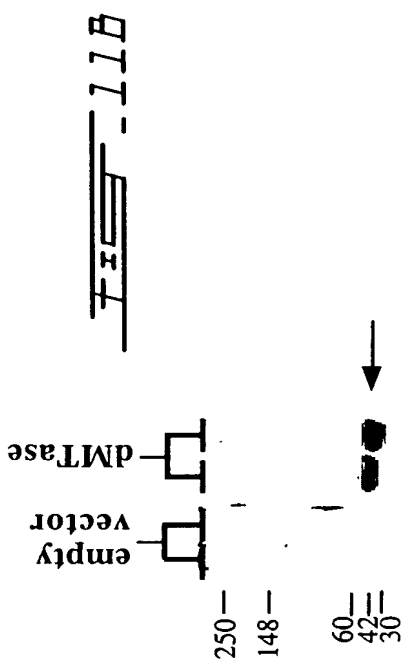


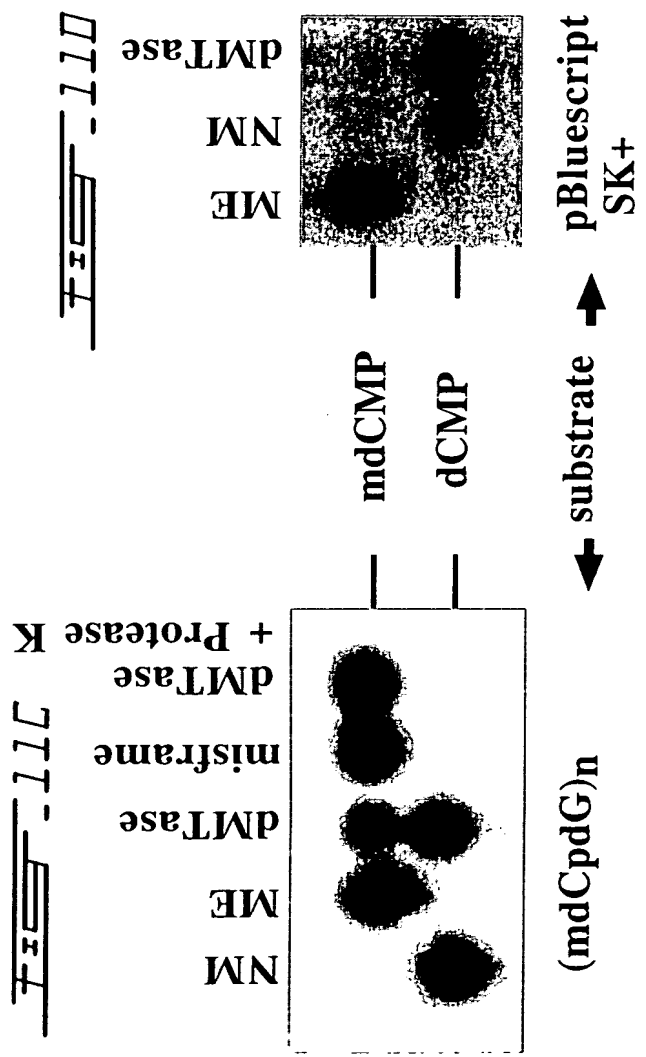
FIG. 11A



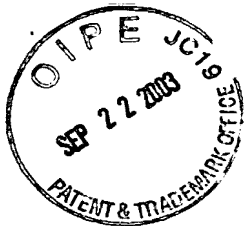
39/50



FrEE-11E  
me SK + Hpa II



0.71  
0.49, 0.40  
0.32  
0.24  
0.15  
dMTase- Buffer L  
dMTase+  
Protease K



40/50

SEP 29 2003

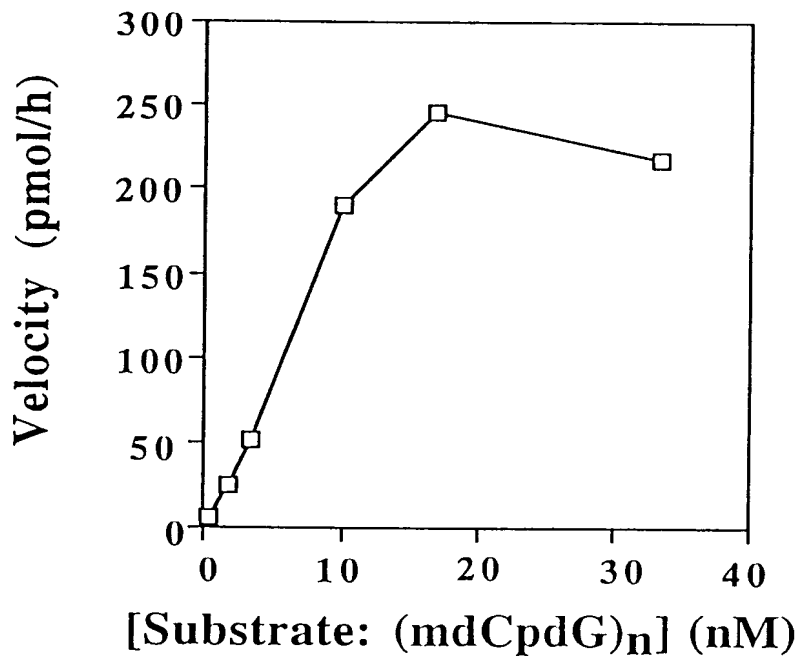


FIG-11F



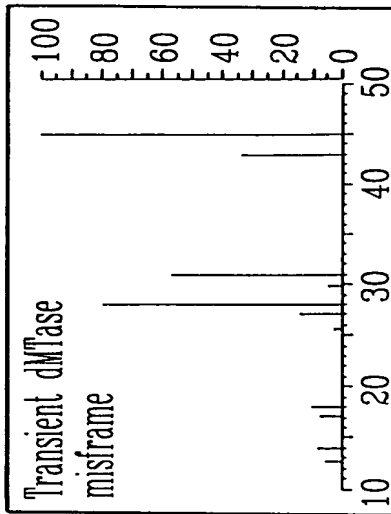
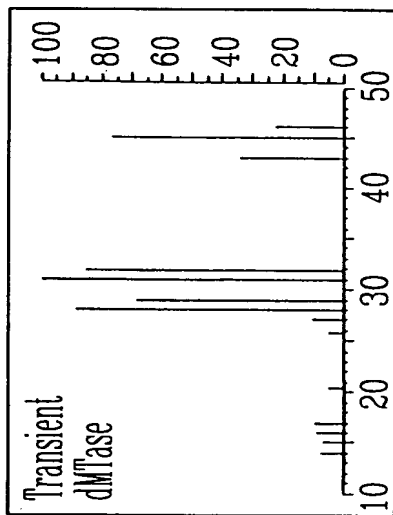
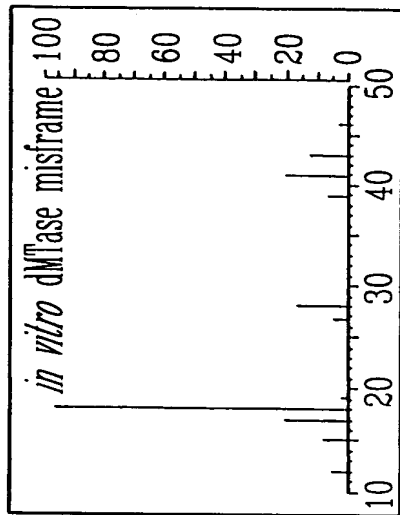
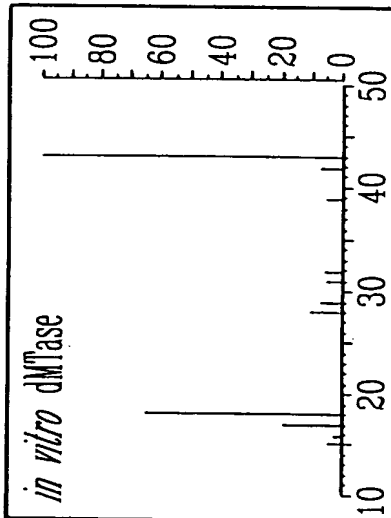
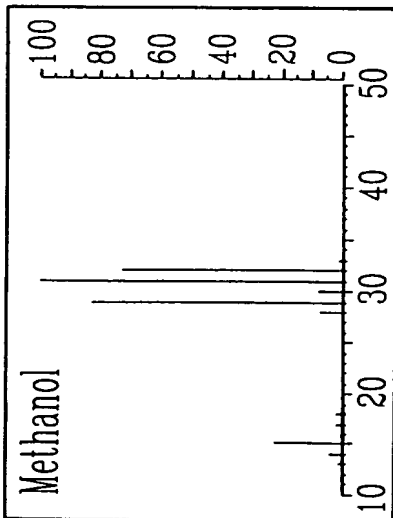
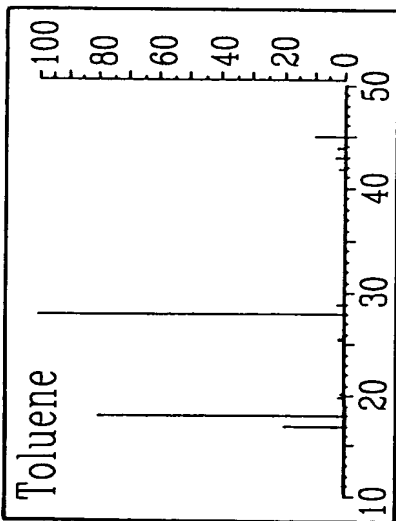
Serial No. 09/554,414  
REPLACEMENT SHEET



42/50

SEP 25 2003

Free - 12B





43/50

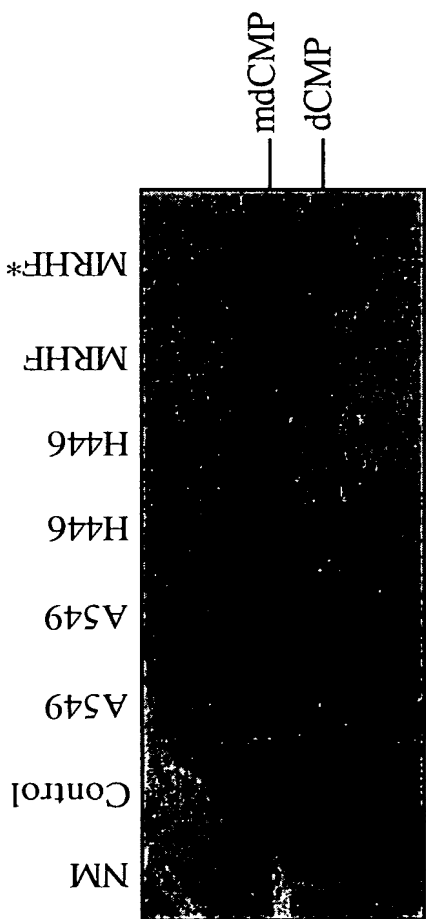
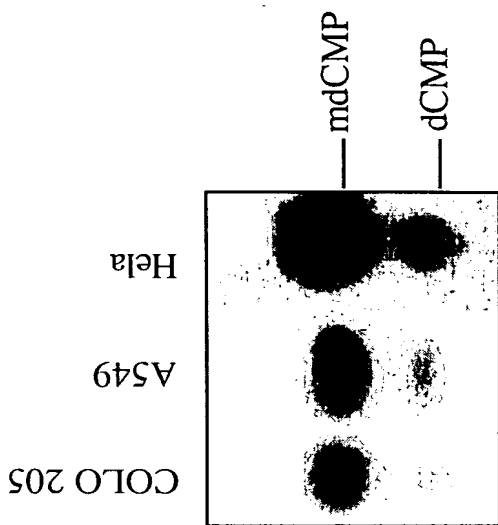
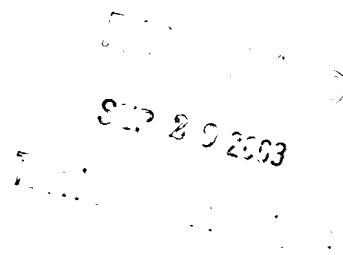


Fig. 13A

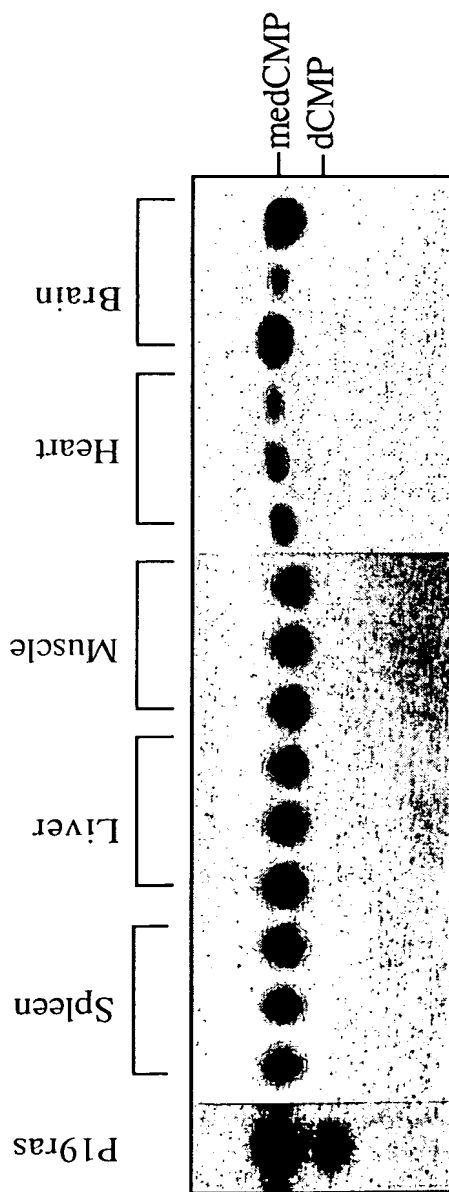
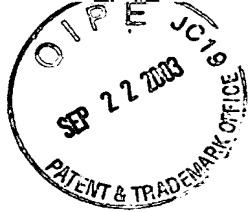


Fig. 13B



44/50

SEP 20 2003

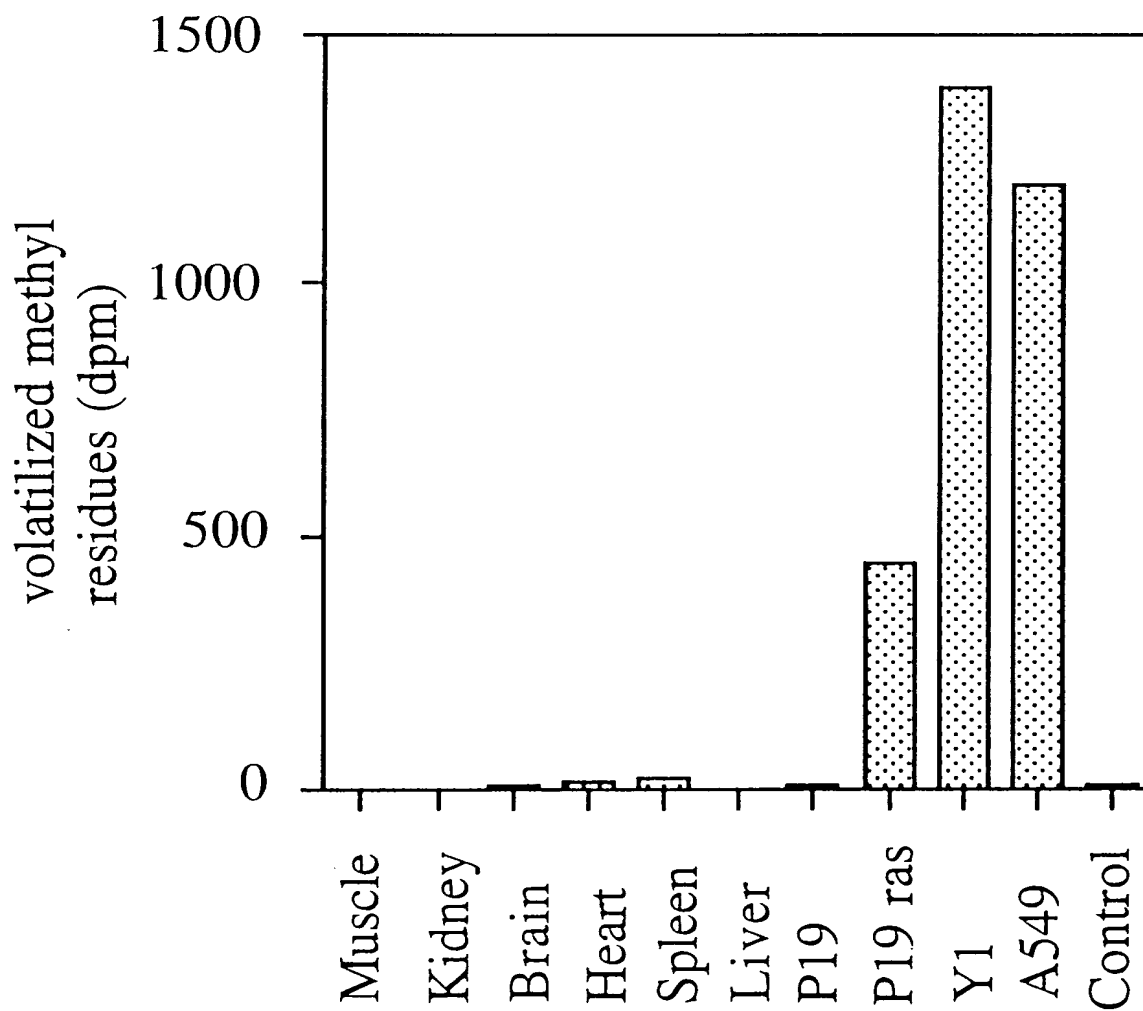
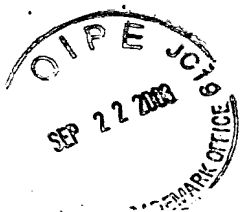


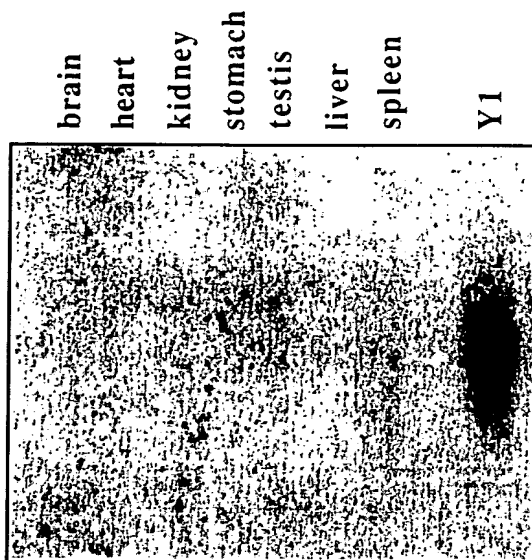
FIG. 13C



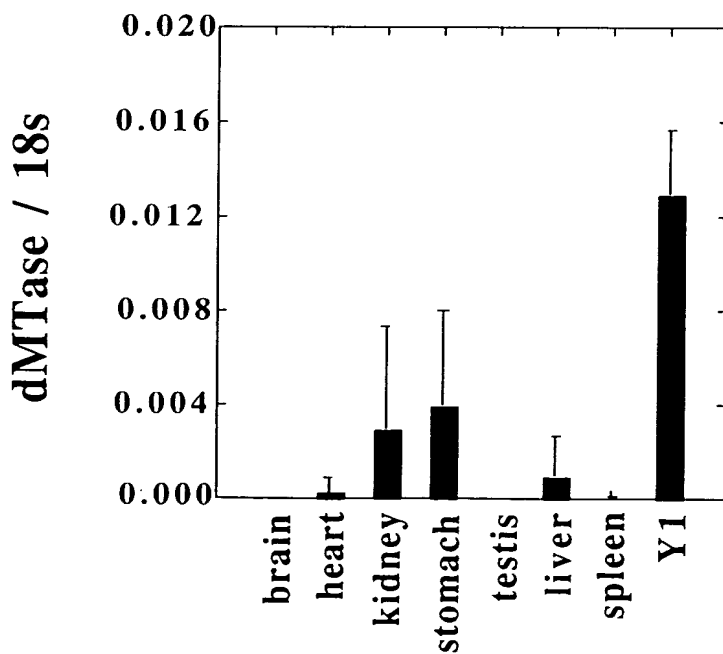
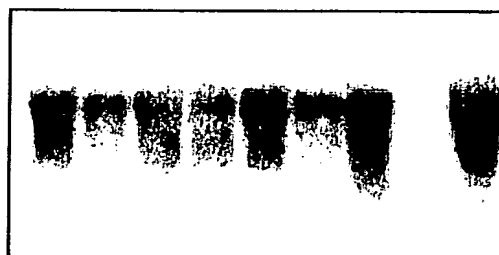
45/50

SEP 20 2003

dMTase



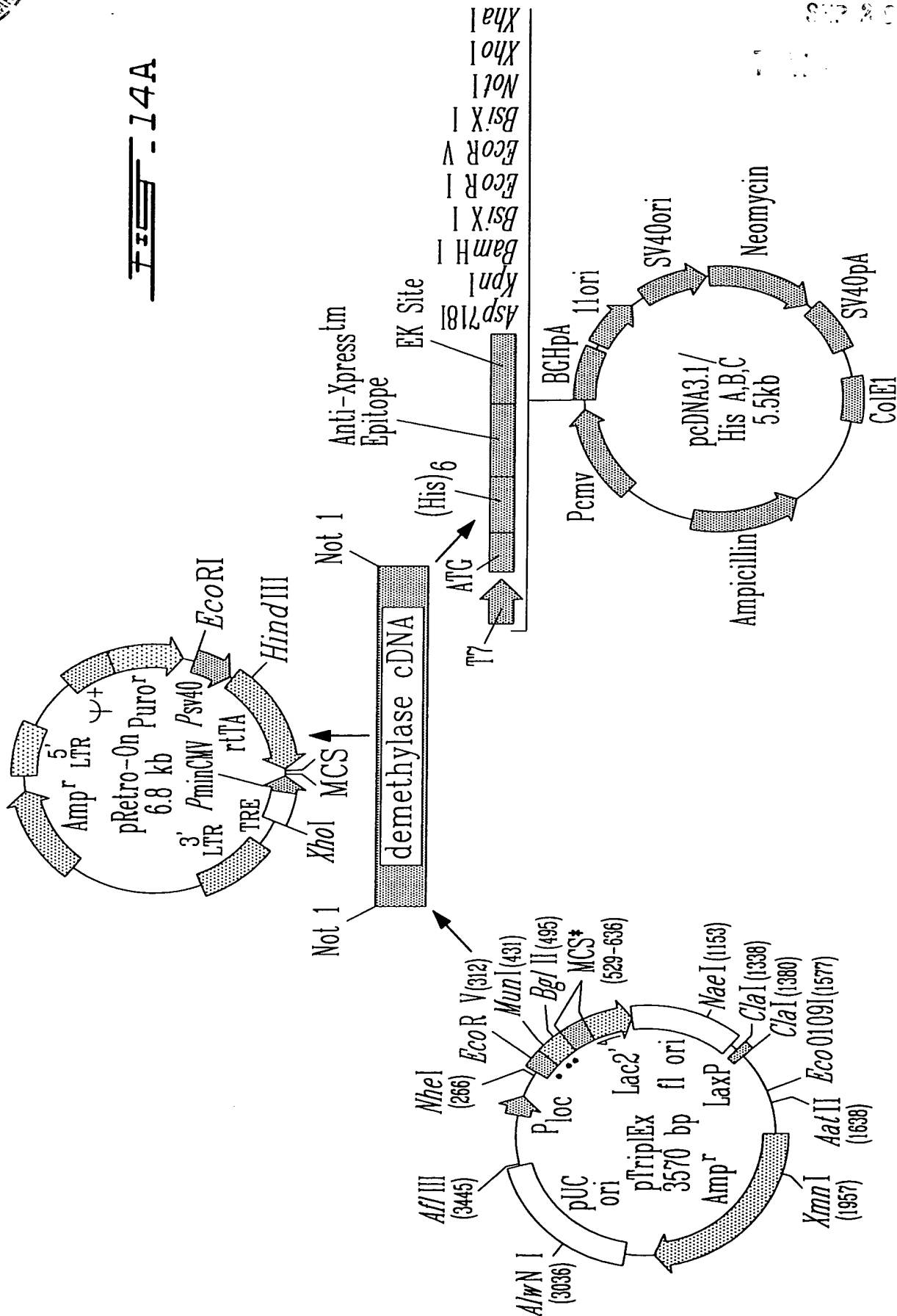
18s



46/50

SEP 22 2003

FIG. 14A





47/50

SEP 22 2003

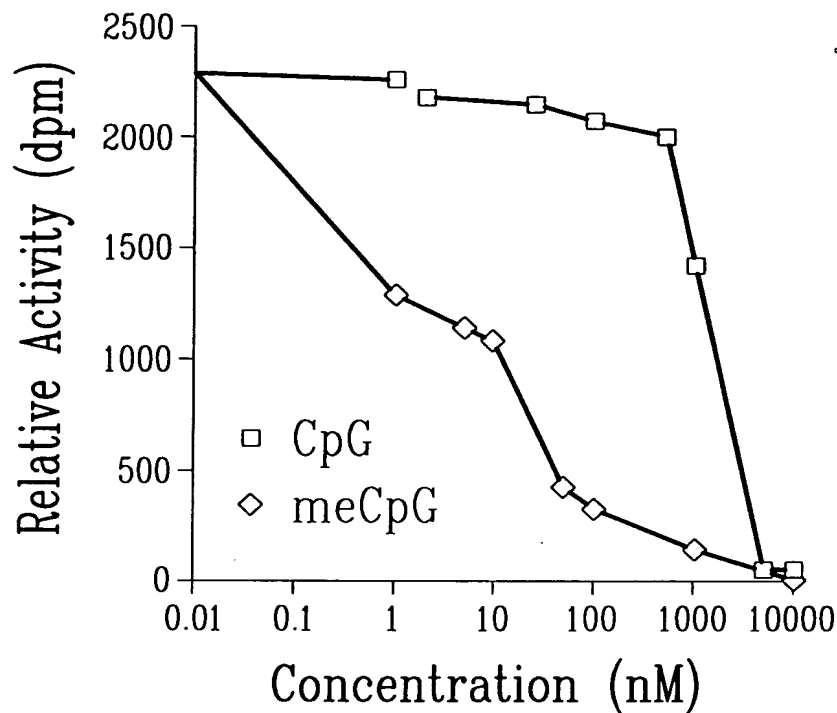


FIG. 14B

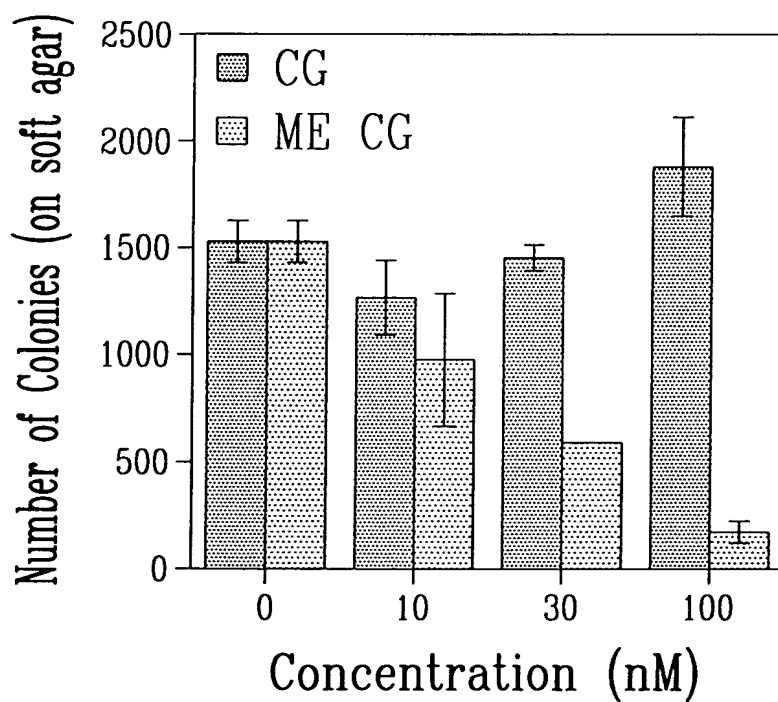
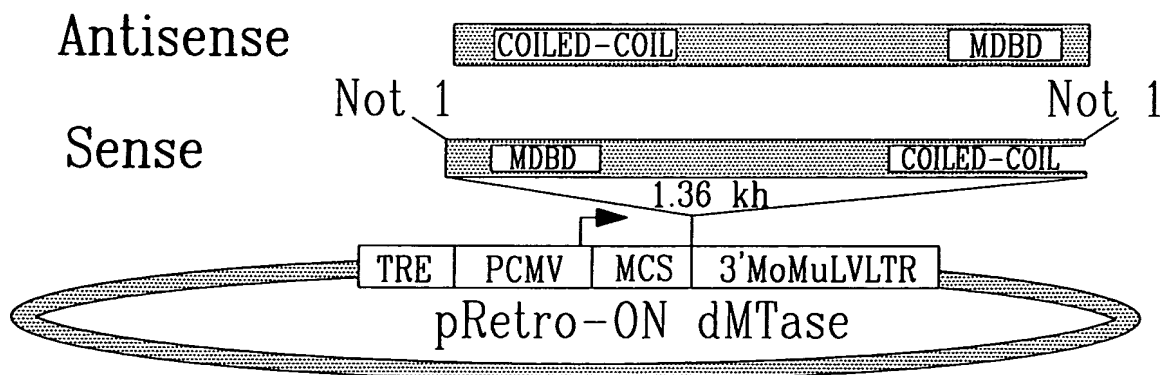
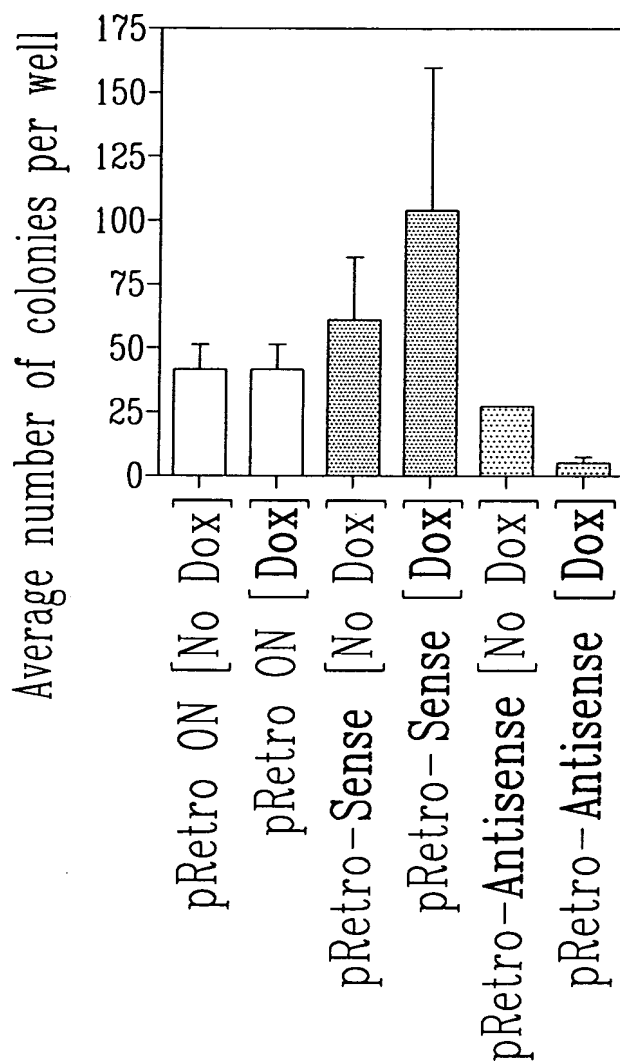


FIG. 14C

48/50

SEP 20 2003







49/50

SEP 20 2003

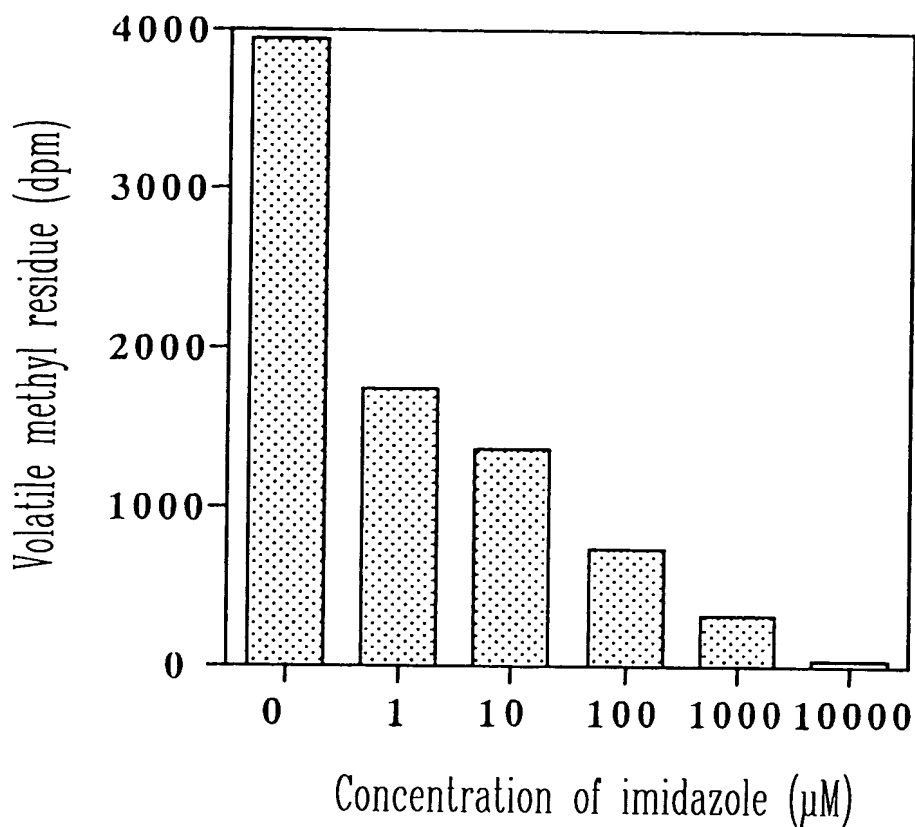


FIG. 16



50/50

SEP 22 2003

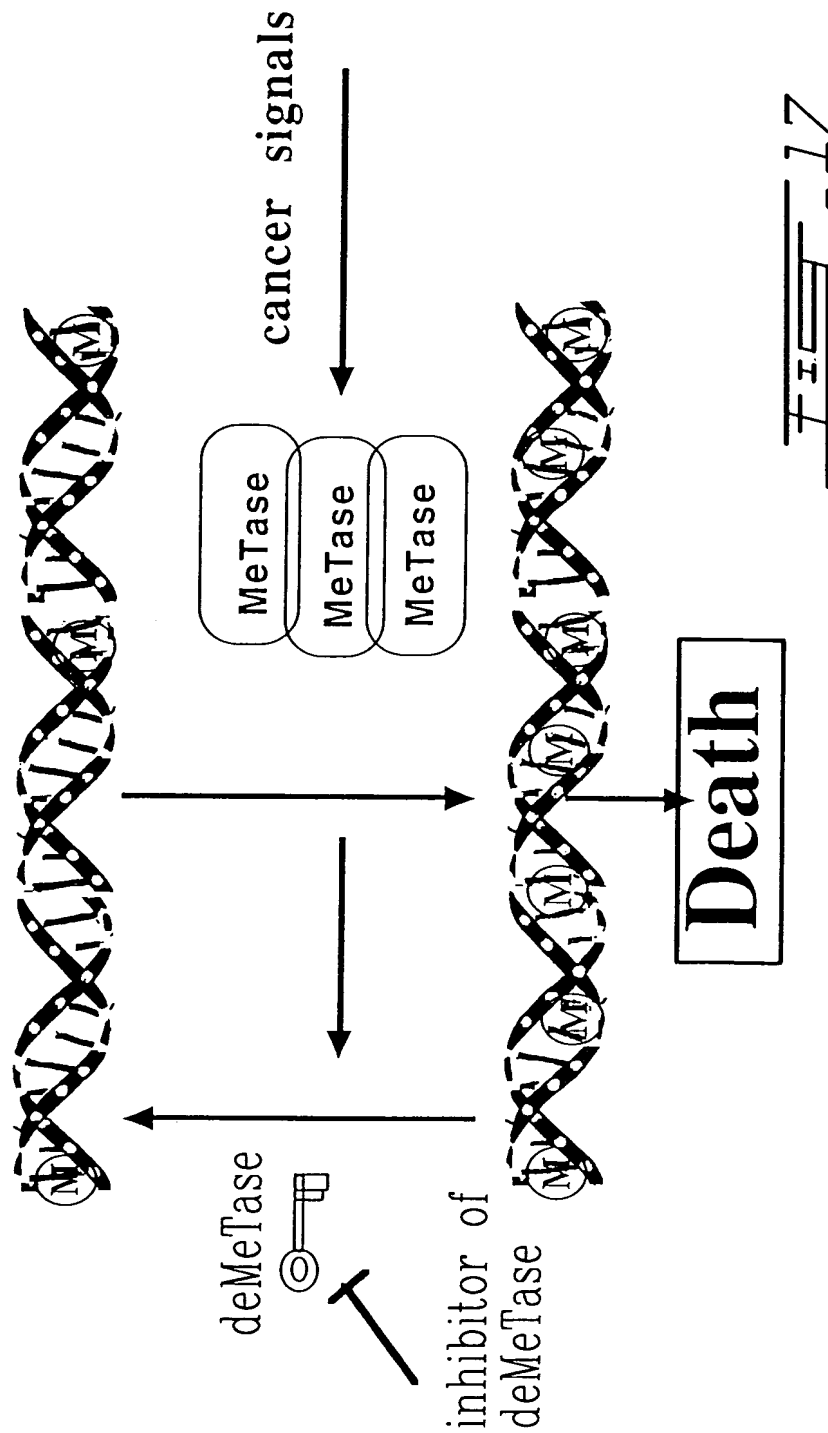


FIG - 17